## STIC-Biotech/ChemLib

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Davis, Natalie

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Natalie A.Davis, PhD Patent Examiner Art Unit 1642 CM1, Rm 8B13 Mailbox 8E12 Ph (703) 308-6410

> Point of Contact Susan Hanley Technical Info. Specialist CM1 6B05 Tel: 305-4053

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
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TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
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Point of Contact Susan Harley Technical Into Specialist CW1 6805 Tek 305-4053 Rattus no Method of

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Esoctto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Fanls, T., Falls, T., Guevara, W., Ganer, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Ganaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hennandez, J., Hernandez, O., Hodgson, A., Hoglas, M., Holloway, C., Hollins, B., Homasl, F., Howard, S., Huber, J., Hillyk, S., Hume, J., Joudah, S., Karatovic, J., Hulber, J., Hillyk, S., Hume, J., Joudah, S., Karatovic, J., Karatovic, J., Lia, Y., Johnson, R., Jolivet, S., Covah, J., Kovar, C., Karatovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. Louiseged, H., Lozado, R.J., Lu, X., Luder, Martindal, A., Maner, G., Martin, R., Martindale, A., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martin, S., Mosey, M., Miner, G., Miner, C., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Nealo, S., Nealow, J., Newtson, J., Newtson, J., Newtson, J., Savery, G., Scherer, S., Scott, G., Shen, H., Shochtari, N., Sisson, T., Sodergren, E., Sonaike, T., Spanks, A., Savery, G., Scherer, S., Scott, G., Shen, H., Shochtari, N., Stone, H., Stutcon, A., Svatek, M., Tameriaa, A., Tameriaa, A., Tameriaa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Tameriaa, A., Tameriaa, A., Tameriaa, K., Walliams, G., Walliams, G., Walliams, C., W
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* NOTE: This is a "working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 127470 bases at least Q40
Consensus quality: 134419 bases at least Q30
Consensus quality: 139475 bases at least Q20
Estimated insert size: 122947; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley, K.C. Department Sequencing Center, Department Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Phrap; version 0.990329First call to findPhrapList
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Contact: hgsc-help@bcm.tmc.edu
------- Project Information
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Summary Statistics
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20-AUG-1999 JP 99P 234764
NAOKI TODO, HAJIME OKUYAMA, MOTOAKI IMAMURA, HIRONORI ISHIKAWA,
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C1201/02,601N33/50,C07K14/47,A61K38/17,C12N5/10,C12P21/02//
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JP 03075332-T/2.
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Eukaryota; Metazoa;
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Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (08-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 5, 2002 this sequence version replaced gi:16077043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheris Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 16553) Sulston,J.E. and Waterston,R.
1482
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HOMO Sapiens BAC clone RP11-32609 from 4, complete sequence.
AC093805 AC012532
AC093805.3 GI:18497223
                                                                        tggttagaagatgcgaatcttcatgtctgtgggaggaagagacggtccaggtcgagaaaa
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Center code: WUGSC
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Cedronl.M., Abbott.A. and Bielicki,L.
The sequence of Homo sapiens BAC clone RP11-32609
Unpublished (2001)
3 (bases 1 to 165538)
Waterston,R.H.
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Waterston, R.H.
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Waterston, R.
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

between neighboring data submissions.

Drafting Center: WIBR

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate

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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                  donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                 The RPCI-11 human BAC library was made from the blood of one male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Data from AC013556 was used to finish the clone, AC093805. Polymorphisms have been identified between AC013556 and AC093805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actual start of this clone is at base position 1 of RP11-32609; actual end is at base position 165538 of RP11-32609.
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1. 165538
Aorganism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
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3627. 3713
//rpt_family="MaLR"
4217. 5074
/rpt_family="AcHobo"
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'590. .7619
/rpt_family="AT_rich"
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/rpt_family="ERV1"

870. .1245

/rpt_family="L1"

1246. .2720
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8315. .9564
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9438. .9470
/rpt_family="(A)n"
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/rpt_family="L1"
7873. .8314
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5385. .5592
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/rpt_family="L1"
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Query Match
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C12Q1/02,G01N33/50,C07K14/47,A61K38/17,C12N5/10,C12P21/02// PC (C12P21/02,C12R1:91)
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                                             Score 695.2; DB 6;
Pred. No. 1.3e-129;
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates;
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                                                  attgtggaagtctcagccccacaacatgatgacatttcagatgaaatttttctacatctc
                                                                                 TATATGGAAGGCTCGCTCCCCATAGCATGACATTTCAAATGAAGTTTTTCTACATATC
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PAT 31-JAN-2002

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1110 bp protein.

BD005226

RESULT BD005226 LOCUS

Method of screening of paper 2226 BD005226.1 GI:18633187 JP 03075332-T/1.

DEFINITION ACCESSION VERSION KEYWORDS

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Todo, N., Okuyama, H., Imamura, M., Ishikawa, H. and Nemoto, K.
Method of screening of protein
L Patent: JP 0375332-T 116-FEB-2001,
SUMITOWO PHARMACEUTICALS CO LTD, NACKI TODO, HAJIME OKUYAWA, OTOAKI
IMAMURA, HIRONORI ISHIKAWA, KIYOMITSU NEMOTO
OS Homo sapiens (human)
PN JP 03075332-T/1
PD 16-FEB-2001
PF 17-AGG-2000 JP 2000005488
PR 20-AGG-1999 JP 99P 234764
PI NACKI TODO, HAJIME OKUYAWA, MOTOAKI IMAMURA, HIRONORI ISHIKAWA,
PI KIYOMITSU NEMOTO
PC C1201/O2/COLN33/50, CG07K14/47, A61K38/17, C120K5/10, C12P21/02// PC
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Catarrhini; Hominidae;
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Pred. No. 4.4e-120;
0; Mismatches 247;
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/db_xref="taxon:9606"
        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1110)
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                                           ctgcttctgatgctgcactatgctgtcgagctcctcccagcgtgtgcagcctgctttac
                                                     aatcggaatggaaatgctctctctgtaatgtcaatgtgttggcagctaaaatcgctgtt
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Direct Submission
Submitted (28-JAN-1992) E. Hartmann, Max-Delbrueck-Centr. J
Molekulare Med., Robert-Roessle-Strasse 10, 0-1115 Berlin I
Location/Qualifiers
1, 2856
/organism="Canis familiaris"
/db_xref="taxon:9615"
/cell_line="MDCK"
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Gorllch,D., Hartmann,E., Prehn,S. and Rapoport,T.A.
A protein of the endoplasmic reticulum involved early in
polypeptide translocation
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/db_xref="SWISS-PROT:Q01685"
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/protein_id="CAA45217.1"
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MTFQMKFFYIAQLAYWFHAFPELYFQKTKKEDIPRQLYYIGIYLFHIAGAYLININHL
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ARABNOKLDSAGNINYLAVRIAVLASICITQAFMMWFINFQLRRWREHSTFQAPVV
ARABNOKLDSAGNINVLAVTSVGADSPRNKKEKSS"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     accetgcagcatggagtcgttgtcc---cagcggaagggctaccetcggggtccaggacc
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Pred. No. 2.2e-99;
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larity 61.5%;
Conservative
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Matches 1183;
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1491
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                                                                                                                              aatggagt-----ggagaatccaaatagaatagattctccaccaaagaagaagag 1542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1689 AATTITIGIATIAGCAAGAIGGCCICTICCAGCAAGGICATITITIAAGITAICTITC 1748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2221
                                                                                                                                                                        aaagc-teettageagttgeaagegaattgattettaeeteeaagggaateeacttette 1601
                                                                                                                                                                                      totttatogaattaacaag-----totgotagcaaagtggtttgttttetcaatgttet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aatattgctaatgtattgtctaatgtgttttaaggttttgcagacgtatgagtggggga
                                                                                                                                                                                                                                                                                                         tgggggttaagactaaaccactcagcct------ctaaatacagtcagaatag
                                                                                                                                                                                                                                                                                                                              1509 TGATTACTATGAGTGAGAAAAATATTTTAGCTTAGACTAAGCTACCTGCCTTCAAAATAG
                                                                                                                                                                                                                                                                                                                                                                                               tgtggtgatgact----gcagaattgtgtacataaataatagtttcctgcttccaatgt
                                                                                                                                                                                                                                                                                                                                                                                                                   1629 IGGAGAGATAACTATTTACAAAATTCTACATAACAGTGATAAAATTTCTTGCTCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cctgcaggataaagtggaaaatctgataaaggttaaactcaaatcagtattatgtaaccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2104 --aaagcatcaaaatatgaatagatgacatgtgtggtgatattgacatttagcgaatcaa
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KASIIFVTLOYNUTLENTEEQATESVSLYYYGIKÖLATVFFYMLVAIIIHAVIQEYML
NEKNIRRENFESKTKHSKFNESQOLSAFTLAKOVATFILISRYISDPTLURRAYPHNL
MTFOMKFFYTSOLAYWHAPPELYFOKTKKEDIPROLVYIGIYLFHTAGAYLIALNH
GLVLLVLHYFVEBELFHSRLFYFFSNEKYQKGFSLWAVLFVLGRLLTLILISVLTVGFGL
ARABENQKLDFSTGNFNYLAYBIAVLASICVTQAFWMKFINFQLRRWREHSAFQAPAV
KKFPYTKGRSKKGTENGVGTLTSNYADSPRNKKEKSS"
4 444 C
4 648 0 9 224 t
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                                     PRI 12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MAIRKKSTKSPPVLSHEFVLQNHADIVSCVAMVFLLGLMFEITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657654. Location/Qualifiers
                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                 Strausberg, R. Direct Submission Submitted (15-NoV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 5 Row: 1 Column: 10
               bccoubs/
Homo sapiens, translocating chain-associating membrane protein, clone MGC:784 IMAGE:3347823, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane
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/organism="Homo sapiens"

/organism="Homo sapiens"

/db_xref="Laxon:9606"

/clone="MGC:784 IMAGE:3347823"

/clone="MGC:784 IMAGE:3347823"

/clone=lib="NHH_MGC_14"

/lab_host="DH10B-R"
                                                                                                                                                                                                                            Homo
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="translocating chain-associating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                             http://mgc.nci.nih.gov
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Pred. No. 3.9e-96;
); Mismatches 598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAH00687.1"
/db_xref="G1:12653797"
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92. .1216
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 2722)
                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                                                                                                     GI:12653796
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61.7%;
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31; Conservative
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                                                                                                                     BC000687.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site:
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Matches 1081;
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ORIGIN
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TITLE
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RESULT
BC000687
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6 9	eggigagiaceggigagiacegeggcaigggeicegcaagaagaacgecaggaacece 49 
125	ccggtgctgagccacgaattcatggtgcagaaccacgcggatatggtctcctgcgtgggc 555 
556	atgitettegtgetgggacttatgitegagggeaeggcegagatgtegategtgiteete 615 
616 245	acctgcagcatggagtcgttgtcccagcggaagggctacctcggggtccaggacc 672 
673 305	ctttaccattatggggtcaaggatctggccacagtgttcttctacatgctggtggccatc 732 
733	atcattcacgccaccattcaggagtacgtgctagataagctcagccggagactgcagctc 792 
793	accaaaggcaaacaaaattgaatgaggccggcagctgagtgttctacatagtg 852 
853 485	tetggtatetggggtatgateattetggeetetgggaetgeetgteagaeeeeaeteta 912 
913 545	ttgtggaagtctcagccacaacatgatgacatttcagatgaaatttttctacatctca 972 
973	cagtiggcitaciggiticatagiticccggagcictaciticcagaaagicaggaaacaa 1032 
1033	gatatcccgggtcaactcatctacattggcctccacctctccacattggagggcctat 1092 
1093	ctcttgtacttgaaccacctgggctgcttctgatgctgcactatgctgtcgagctc 1152 
1153 785	ctctccagcgtgtgcagcctgctttactttggggatgaggggtaccagaaagggttgtct 1212 
1213	ttgtggcctatcgtgtttatatccgggagactcgtgacactgattgtctcagtggttaca 1272 
1273 905	gtaggettcacttggccgggacaaatcggaatggaaatgctctctctggtaatgtc 1329 
1330	aatgigitggcagctaaaatcgctgttctgtcctcgagttgcagtatccaggtgtacata 1389 
1390	acatggaccttgacgaccgtctggcttcagagatggttagaagatgcgaatcttcatgtc 1449 
1450	tgtgggaggaagagacggtccagg             CCAGCTGTGAAGAAACCAACAGTAA

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Young P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D. R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature gene sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT 09-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                             1619
                                                                                                                                                                                                                                                                                                                                                                                         1679
aatggagtggag-----aatccaaatagaatagattctccaccaaagaagaagag 1542
           ttatgtggtgtctctgtgctagagattttctgttcttcagaacgggtcgtgcttttgaa 1661
                                                                                                               1265 CTATATCTTTCAGCATTAGAGATTTTTCTGTTGAAAATACAGTCTGTGCTCTTTGAT 1324
                                                                                                                                     tattgctaatgtattgtctaatgtgtttttaaggttttgcagacgtatgagtgggggatg 1721
                                                                                                                                                   1722 ggggttaagactaaaccactcagcct-------ctaaatacagtcagaatagtt 1768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1560 ITITIATAATAGCAGAGTGGCCTGTICTAAGAAGGCCATATTTTTAAGTTATCTTTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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/db_xref="taxon:9606"
278 c 275 q 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAAAAACATAA 1810
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AX329795
LOCUS
DEFINITION
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VERSION
KEYWORDS
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      Score 493.8; DB 6;
Pred. No. 4.3e-89;
0; Mismatches 387;
      21.4%;
Query Match
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1267)
Todo, N., Okuyama, H., Imamura, M., Ishikawa, H. and Nemoto, K.
Method of screening of protein
L Patent: JP 03075332-T 4 16-FEB-2001;
SUMITOMO PHARMACEUTICALS CO LTD, NAOKI TODO, HAJIME OKUYAMA, OTOAKI
IMAMURA, HIRONORI ISHIKAWA, KIYOMITSU NEMOTO
OS Homo sapiens (human)
PN JP 03075332-T/4
PD 16-FEB-2001
PF 17-AUG-2000 JP 2000005488
PR 20-AUG-1999 JP 99P 234764
PI NAOKI TODO, HAJIME OKUYAMA, MOTOAKI IMAMURA, HIRONORI ISHIKAWA,
PI KIYOMITSU NEMOTO
PC C1201/O2.GOIN33/50.CO7K14/47, A6IK38/17, C12N5/10, C12P21/02// PC
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

human.

ORGANISM

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KKRPTYTKGRSSKKGTBNGVATLSNVADSPRNKKEKSS"
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                                                                                                                                                    Direct Submission
Submitted (28-JAN-1992) E. Hartmann, Max-Delbrueck-Centr.
Molekulare Med., Robert-Roessle-Strasse 10, 0-1115 Berlin
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTGCAGCGGGGCCGTGACCAGCAGCCAGCGGAGGCGGCGGCGAGTCGGTGAGCAGCT
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            1 (bases 1 to 1267)
Gorlich,D., Hartmann,E., Prehn,S. and Rapoport,T.A.
A protein of the endoplasmic reticulum involved early
Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
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Pred. No. 4.3e-89;
); Mismatches 387;
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122. .1246
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Nature 357 (6373), 47-52 (1992)
92244357
2 (bases I to 1267)
Hartmann, E.
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65.78;
Eutheria;
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Sequencing by: Baylor College of Medicine Human Genome
                                                           Contact: villalon@bcm.tmc.edu.
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66.2%;
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                 Sequencing Center
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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clone MGC:11724 IMAGE:3967323, mRNA, complete cds
                                                                                                                                                                          tctacttccagaaagtcaggaaacaagatatcccgggtcaactcatctacattggcctcc 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atggaaatgctctctctggtaatgtcaatgtgttggcagctaaaatcgctgttctgtcct 1363
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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BC012401
BC012401.1 GI:15214554
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AUTHORS
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JOURNAL
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KEYWORDS
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/dc_xref="G1:15214555"
/dc_xref="G1:1521455"
/dc_xref="G1:15
                                                                                                                                                                                                                                                                                                                                                      found
                                                                                                                                                    Garcia,
                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 17 Row: j Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy." /clone_lib="NCL_CGAP_Maml" /lab_host="DH10B"
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                                                                                                                                    Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., G
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu,
Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGAGCCATCATCTTGTTGCTCTTCAGTATAATGTTACCCGCCCTGCAACAGAACA
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Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Pred. No. 1.9e-87;
0; Mismatches 370;
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/db_xref="taxon:10090"
/clone="MGC:11724 IMAGE:3967323"
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Clark.T.G., Morris,J., Akamatsu,M., McGraw,R.A. and Ivarie,R.D.
Cloning and sequence analysis of a bovine tram cDNA
Unpublished
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Clark,Tu.G., Morris,J., Akamatsu,M., McGraw,R.A. and Ivarie,R.D.
Direct Submission
Submitted (06-JAN-1995) Genetics, University of Georgia, Athens
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                                                                                 /product="translocation chain-membrane
                                                                                                                                                                                                                                                                   Score 481.6; DB 4;
Pred. No. 1.4e-86;
0; Mismatches 419;
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64.0%;
                                   /gene="tram"
<1. .1077
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/protein_id="Aak38167.1"
/dc_xxef="d1:13774095"
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BYNIRRHFEKTKHRSKTRSCOLSAFYLFACWYGTFLLISRNYISPPTILKRAYPHNL
MTFQTKFFYISQLAYMLHAFPELYFKKTKEDIPRQLVYIGLYLFHIAGAYLLNLNHI
GLVLLVHTYFVEFLFHISRLFFFSDEKYQKGFSLMANLFVLGELXLFHIAGAYLLNLNHI
GLVLLVHYFVEFFFHISRLFFFSDEKYQKGFSLMANLFVLGELLTLLSVLTVGFGB
ARABNOKLDFGTGNFNVLANTAVLASICITYQAFMMKFINFQLRRWREHSAFQAPPY
ARRANYTKGRSSRKGTENGVGTVISNGADSPRNRKEKSS"
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Sciurognathi; Muridae; Murinae; Mus
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Submitted (09-APR-2001) Biologie,
Allee 160, Luebeck 23538, Germany
Location/Qualifiers
1. .2720
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Mammalla; Eutheria; Rodentia;
1 (bases 1 to 2720)
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TITLE
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                            9
                             Indels
  10;
              4.1e-86;
  DB
                            0; Mismatches
Score 479.4;
Pred. No. 4.1
Query Match 20.7%;
Best Local Similarity 67.2%;
Matches 710; Conservative
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ggccgggcagctgagtgttctacatagtgtctggtatctggggtatgatcattctggc
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SOURCE
ORGANISM
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AUTHORS
  822
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AY029529
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                                                                                                                                                                                  02-MAY-2001
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 1338)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratzeburger
969 ATGTGGAAGTTCATTAACTTCCAGCTTCGGAGGTGGAGGGAACATTCTGCCTTCCAGGCC 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catggggctccgcaagaagaacgccaggaacccccggtgctgagccacgaattcatggt
                                                                                                                                                                                    VRT
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Pred. No. 5.6e-78;
0; Mismatches 399
                                                                                                                                                                                Xenopus laevis Tram1 mRNA, complete cds. AY029534
                                                               tgtgggaggaagacggtccaggtcgagaaaggca
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/db_xref="taxon:8355"
/clone="R2PD A01802Q2"
16. .1137
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Submitted (10-APR-2001) Biologie,
Allee 160, Lubeck 23538, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="Tram1"
/protein_id="AAK40302.1"
/db_xref="GI:13936287"
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63.2%;
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Best Local S.
Matches 691
                                                                                                                                                           AY029534
LOCUS
DEFINITION
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ORIGIN
                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                         ORGANISM
                                        1450
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AUTHORS
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JOURNAL
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1 (bases 1 to 1453)

Hartmann, E.
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                                                                                                                                                                 942 gacatttcagatgaaatttttctacatctcacagttggcttactggtttcatagtttccc 1001
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                    434
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                                                                      ctctgagaactgcctgtcagaccccactctattgtggaagtctcagccccacaacatgat
                                                                                                                                                                                           University Lubeck,
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Submitted (09-APR-2001) Biologie,
Allee 160, Lubeck 23538, Germany
Location/Qualifiers
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/organism="Danio rerio"
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This sequence represents the DNA encoding an endoplasmic reticulum protein (WAR-1). The invention includes rat and human WAR-1 sequences, expression vectors containing the DNA, cells transformed with the expression vector, antibodies against WAR-1, and probes and primers which hybridise to the DNA encoding WAR-1. The WAR-1 protein inhibits the proliferation of cancer cells, and is used in the treatment and diagnosis of cancers including highly malignant sarcomas. ö 120 180 180 240 240 300 300 360 360 480 540 420 420 480 540 900 900 099 Gaps 099 720 780 840 9 9 gtctcctgcgtgggcatgttcttcgtgctgggacttatgttcgagggcacggcgagatg, gctccttaagggaaggtgagattcctaagagatcagtagagagcaccagggagctcgctg ctgtgttgctatggtgatgatggcaatggtaatgacagtggcaccagatttccctgttcc aacgccaggaacccccggtgctgagccacgaattcatggtgcagaaccacgcggatatg ctgcgaccctgggcggcagacgggcggggatggggagcccggcgctgggagcggcagt gatcagcggtggccggtgagtaccggtgagtaccgcgggcatggggctccgcaagaag gtctcctgcgtgggcatgttcttcgtgctgggacttatgttcgagggcacggccgagatg ctggtggccatcatcatcacgccaccattcaggagtacgtgctagataagctcagccgg agactgcagctcaccaaaggcaaacaaaacaaattgaatgaggccgggcagctgagtgtg ö Length Indels other; 21; .; 0 T; 0 DB 602 Score 2311; Pred. No. 0; ; Mismatches 608 A; 502 C; 599 G; ; Japanese Local Similarity 100.0%;
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                                                                                                                                      attaaagcatcaaaatatgaatagatgacatgtgtggtgatattgacatttagcgaatca
                                                                                                                                                                                                                    Transformation of a cell with separate vectors expressing the antisense strands of WAR-1 DNA for screening secretory and memproteins expressed by the cell
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                                                                                                                                                     membrane proteins consisting of transformation of a cell with separate expression vectors for the sense and antisense RNA of DNA encoding an endoplasmic reticulum membrane protein participating in endoplasmic reticulum transport of proteins. Also described are: (1) secretory and cell membrane proteins identified by the screening method; (2) drug compositions containing these proteins; (3) host cells transformed by the separate expression vectors of the method; and (4) the preparation of secretory and cell membrane proteins by culture of the transformants. The method can be used for the identification and preparation of proteins for use in the treatment and prevention of diseases such as cancer, disorders of the nervous system, immune disorders (including allergies and rheumatism) and skeletal disorders. The present sequence encodes a specifically claimed rat WAR-1 protein from the present
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100.0%; Pred. No. 2.4e-202;
ive 0; Mismatches 0;
Page 65-68; 79pp; Japanese.
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Okuyama H;
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                                Length 2288
                                                     Indels
 other;
                              Score 802.2; DB 21;
Pred. No. 3.9e-146;
); Mismatches 563;
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706
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467
                              34.7%;
68.2%;
 612 A;
                                                       Conservative
                                         Best Local Similarity
Matches 1418; Conserv
 BP;
 2288
  Sequence
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2202 ctgccatatatttgcatcaaaatatcattaattat

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tggatcgcagaatcggaatcctgatgcccttactggaaatgtaaatgttggcagctaa 1366
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The can gene at also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving a quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the printed and produce other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human confidence data for this patent did not appear in the printed specification, in the printed specification, in the printed specification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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                                                                                                                            novel human diagnostic protein #12225.
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0; Mismatches 519;
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                    ВР
                  AAS76421 standard; cDNA; 1835
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2000US-0649167
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                                                                                        (first entry)
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Best Local Similarity
Matches 1268; Conserv
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                                                                                                                                                                                                                                                      WO200175067-A2.
                                                                                                                          DNA encoding
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23-AUG-2000;
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Qy	523	agaaccacgcggatatggtctcctgcgtgggcatgttcttcgtgctgggacttatgtt	
qq	61	cagaatcatgoggacatcgtctcctgcgtggggatgttcttcctgctggggcttgtgttc 120	
Qy Db	583	gagggcacggcgagatgtcgatcgtgttcctcaccctgcagcatggagtcgttgtcc 640 	
Oy Db	641	-cagoggaagggctaccctcggggtccaggaccctttaccattatggggtcaaagatctg 699 	
Oy Db	700	gccacagtgttcttctacatgctggtggccatcatcatcacgccaccattcagagtac 759 	
Qy	9 0	toctagataagctcagcoggagctgcagctcaccaaaggcaaacaaaaca	
Qy Dp	361	atagtgtctggta             ttttttcttgta	
Qy	880	gcctctgagaactgcctgtcagacccactctattgtgaagtctcagccccacaacatg 939 	
Qy Dp	940	atgacatttcagatgaaatttttctacatctcacagttggcttactggtttcatagtttc 999 	
Qy	1000	coggagototacttocagaaagtoaggaaacaagatatocoggtoaactoatotacatt 1059 	
Qy	1060	ggcctccacctctccacattggagggcctatctcttgtacttgaaccacctgggcctg 1119 	
Qy Db	1120	ctgcttctgatgctgcactatgctgtcgagctcctccagogtgtgcagcctgctttac 1179 	
Qy	1180	ttiggggatgagcggtaccagaaagggttgtctttgtggcctatcgtgtttatatccggg 1239 	
Qy Db	1240	agactcytgacactgattgtctcagtggttacagtagggcttcacttggccgggaca 1296 	
O <sub>Y</sub>	1297 841	aatoggaatggaaatgctctctggtaatgtcaatgttggcagctaaaatcgctgtt 1356 	
Oy Ob	1357 901	ctgtcctcgagttgcagtatccaggtgtacataacatggaccttgacgaccgtctggctt 1416 	
δ O	1417 961	cagagatggttagaagatgcgaatcttcatgtctgtgggaggaagaga 1464 	
Qy	1465	cggtccaggtcgagaaaaggcacagaaatggagtggagaatccaaatagaatct 1524 	
Q.y D.b	1525	ccaccaaagaagaaagagaaagctccttagcagttgcaagcgaattgattcttacctcca 1584 	

1585 agggaatccacttcttcttatgtggtgtctctgtgctagaga-ttttctgttcttcagaa 1643 agt----ttcctgcttccaatgttctttatcgaattaacaagtctgctagcaaagtggt 1915 tgccatatattgcatcaaaatatcattaattaatataaaaatttaaaatcattcctg 1786 -----aaggttttgcagacgtatgagtgggggatgggggttaagactaaaccactcag 1744 atcagtattatgtaaccgttgggatttttttaaagtgttttaaatttacaatggaaagca 2035 tttgtcaaaccacca-aaaatatgtgtttaattttatgagtagtaattgttagtgcttac 2094 ttgttttctcaatgttctcctgcaggataaagtggaaaatctgataaaggttaaactcaa gaatcaagatacctttaataaatatggtgggttactaaagaagtaaacgacttcttcctg full length cDNA; cDNA synthesis; oligo-capping; ss. Human full-length cDNA, SEQ ID NO: 2724. BP AAK94181 standard; cDNA; 1736 08-JUL-1999; 99JP-0194486. 11-JAN-2000; 2000JP-0118774. 02-MAY-2000; 2000JP-0183765. 07-JUL-2000; 2000EP-0114089 06-NOV-2001 (first entry) Homo sapiens EP1130094-A2 05-SEP-2001 AAK94181; Human; Ŋ 1141 1318 1378 1258 1801 1861 1916 1498 1976 1556 2036 1616 2155 1727 1692 1745 AAK94181 g Óλ g g ολ g g g οy q δ q qq δ g qq ٥y Ω οy δŽ ŏ οy g 

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                                                                                                                                                                            The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3' ends of the CDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.
                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                             their
                                         H;
                            Kawai Y;
T, Koga
                                                                                                           Claim 8; SEQ ID NO 2724; 1380pp + sequence listing; English.
                           Ishii S,
S, Otsuki
                                                                                                                                                                                                                                                                                                                                                             Sequence 1736 BP; 448 A; 358 C; 390 G; 540 T; 0 other;
                           Hayashi K,
K, Kojima
                       Isogai T, H
na T, Nagai F
                                        Wakamatsu A, Sugiyama T,
(HELI-) HELIX RES INST
                           Nishikawa T,
                                                                  2001-524255/58
                                                                 WPI; 2001-524255,
P-PSDB; AAM93265
                                                                                                            830
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8 215 275 614 335 671 731 455 515 851 554 791 Gaps 157 gccggtgagtatccggga-agcgccaccatggggctccgtaagaagagcaccaagaaccc caccetgcagcatgqagtegttgtce--cagcggaagggetacectgggggtccaggac 336 cactetteageacagtgttgetgteetgeageageaggaacaageeacgggeteaaagte 792 caccaaaggcaaacaaaacaaattgaatgaggccgggcagctgagtgtgttctacatagt gccggtgagtaccggtgagtaccgcgtgaggggtccgcaagaagaacgccaggaaccc cccggtgctgagccacgaattcatggtgcagaaccacgcggatatggtctcctgcgtggg catgitettegigetgggaettatgitegagggeaeggeegagatgtegategigtteet catcattcacgccaccattcaggagtacgtgctagataagctcagccggagactgcagct cattattcatgccacaattcaggaatatgtgttggataaaattaacaagagaatgcagtt 46; Length 1736 0; Mismatches 363; Indels 31.1%; Score 718.2; DB 22; 72.2%; Pred. No. 6.9e-130; Query Match
Best Local Similarity 72.23
Matches 1062; Conservative 435 495 615 732

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protein;
                                       tctcttgtacttgaaccacctgggcctgctgcttctgatgctgcactatgctgtcgagct
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The present invention describes a screening method for secretory and membrane proteins consisting of transformation of a cell with separate expression vectors for the sense and antisense RNA of DNA encoding an endoplasmic reticulum membrane protein participating in endoplasmic rediculum transport of proteins. Also described are: (1) secretory and cell membrane proteins identified by the screening method; (2) drug compositions containing these proteins; (3) host cells transformed by the separate expression vectors of the method; and (4) the preparation of secretory and cell membrane proteins by culture of the transformants. The method can be used for the identification and preparation of proteins for use in the treatment and prevention of diseases such as cancer, disorders of the nervous system, immune disorders (including allergies and rheumatism) and skeletal disorders. The present sequence encodes a specifically claimed human WAR-1 protein from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transformation of a cell with separate vectors expressing the sense and antisense strands of WAR-1 DNA for screening secretory and membrane
cell membrane protein; cytostatic; CNS active; antiallergic; cancer; antirheumatic; nervous system disorder; immune disorder; allergy; rheumatism; skeletal disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishikawa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 68-71; 79pp; Japanese.
                                                                                                                                                                                                       Location/Qualifiers
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74.98;
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P-PSDB; AAB70695.
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                                                                                                                                               Homo sapiens
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9 gccggtgagtaccggtgagtaccgcggcatggggtccgcaagaagaagacgccaggaaccc 494 554 191 731 Gaps 13 geoggtgagtateoggga-agegecaceatggggeteogtaagaagageaceagaacec 71 cctttaccattatggggtcaaagatctggccacagtgttcttctacatgctggtggccat cccggtgctgagccacgaattcatggtgcagaaccacgcggatatggtctcctgcgtggg catgttcttcgtgctgggacttatgttcgagggcacggccgagatgtcgatcgtgttcct caccetgcagcatggagtcgttgtcc---cagcggaagggctaccetcggggtccaggac 23; DB 22; Length 1288; Indels Score 695.2; DB 22; Pred. No. 1.8e-125; ); Mismatches 298; Best Local Sin Matches 957; Query Match 435 72 132 515 495 555 192 672

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1091 cctctccagcgtgtgcagcctgctttactttggggatgagcggtaccagaaagggttgtc 1211 gttgcaagcgaattgattettacetecaagggaatecaettettettatgtggtgtetet 1616 731 971 tatatggaaggctcgtccccatagcatgatgacatttcaaatgaagtttttctacatatc caatgtgttggcagctaaaatcgctgttctgtcctcgagttgcagtatccaggtgtacat cctctattattatggtgtcaaagatttggccacggttttcttctacatgctggtggcaat agatatecegggteaaeteatetaeattggeeteeaeetetteeaeattggaggggeeta tctcttgtacttgaaccacctgggcctgctgcttctgatgctgcactatgctgtcgagct tttgtggcctatcgtgtttatatccgggagactcgtgacactgattgtctcagtggttac agtagggetteaettggeegg---gacaaateggaatggaaatgetetetetggtaatgt catcattcacgccaccattcaggagtacgtgctagataagctcagccggagactgcagct gtctggtatctggggtatgatcattctggcttctgagaactgcctgtcagaccccactct 432 ttcttgtattttggggcacattcattttaatctctgaaaactgcctgtcagacccaactct attgtggaagtctcagccccacaacatgatgacatttcagatgaaatttttctacatctc 852 tgttgggtttcacctggctggatcgcagaatcggaatcctgatgcccttactggaaatgt 912 aaatgigitggcagctaaaattgctgitctgicgiccagtigcacgaiccaagcctacgi ctgtgggaggaa-----gaagacggtccaggtcgagaaaggcacagaaatgg ctcatgtatgaaaaagaaacggtcgagatcttctaaaaaaagaacagaaacggagtggg ||| | |||| ||||| ||||| || tgtttcatgtattttta 1286 tgtctaatgtgtttttaa 1693 492 372 1032 612 1092 672 1152 1212 1272 1389 972 1449 1032 1497 1092 1557 1152 1617 1676 732 312 792 852 792 1209 1269 ò g g ò g ŏ qq õ g ò g δ g δ В δ g δ g Qγ q ò g ŏ g òγ Óλ g 셤 ŏ δλ

RESULT AAF74780

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The present invention describes a screening method for secretory and membrane proteins consisting of transformation of a cell with separate expression vectors for the sense and antisense RNA of DNA encoding an endoplasmic reticulum transport of proteins. Also described are: (1) secretory and cell membrane proteins identified by the screening method; (2) drug compositions containing these proteins; (3) host cells transformed by the separate expression vectors of the method; and (4) the preparation of secretory and cell membrane proteins by culture of the transformants. The method can be used for the identification and preparation of proteins for use in the treatment and prevention of diseases such as cancer, disorders of the nervous system, immune disorders (including allergies and rheumatism) and skeletal disorders. The present sequence
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                                                                                                                                   endoplasmic reticulum membrane transportation; secretory protein; cell membrane protein; cytostatic; CNS active; antiallergic; cancer; antirheumatic; nervous system disorder; immune disorder; allergy;
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                                                                                                                      protein screening; endoplasmic reticulum
                                                                                        Human WAR-1 encoding cDNA sequence SEQ ID NO:3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 62-65; 79pp; Japanese.
                                                                                                                                                                                                                                            ocation/Qualifiers
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                                                                                                                                                                                   rheumatism; skeletal disorder; ss
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   BP.
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AAF74780 standard; cDNA; 1110
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P-PSDB; AAB70695.
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                                                          17-MAY-2001
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                              AAF74780;
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961
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                                                                                         1 atggggctccgtaagaagagcaccaagaaccccccgttctcagccaggaattcatcctg
                             DB 22; Length 1110;
                                                  18;
                                                  Indels
                           Score 647.8; DB 22;
Pred. No. 2.7e-116;
0; Mismatches 247;
                            28.0%;
76.1%;
                                      Best Local Similarity 76.1
Matches 844; Conservative
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Query Match

463

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523 61

1179 1239 1416 ccggagetctacttccagaaagtcaggaaacaagatatcccgggtcaactcatctacatt 1059 agactogtgacactgattgtctcagtggttacagtagggcttcacttggccgggac---a 1296 1464 cagaggtgggtagaagattctaatattcaggcctcatgtatgaaaaagaaacggtcgaga 1020 1021 tettetaaaaaaaagaacagaaaaeggaagtgggaagtggaaaeetteaaatagagtagaetgt 1080 9 180 ggcctccacctcttccacattggagggcctatctcttgtacttgaaccacctgggcctg atctctgaaaactgcctgtcagacccaactcttatatggaaggctcgtccccatagcatg -cagoggaagggctacctcggggtccaggacctttaccattatggggtcaaagatctg gcagcagaggaacaagccacgggctcaaagtccctctattattatggtgtcaaagatttg gtgctagataageteageeggagactgcageteaceaaaggeaaacaaaattgaat gaggccgggcagctgagtgtgttctacatagtgtctggtatctggggtatgatcattctg gootetgaagaactgcctgtcagaccccactctattgtggaagtctcagccccacaacatg atgacatttcagatgaaatttttctacatctcacagttggcttactggtttcatagtttc ggtcttcacctcttccacattactggagcttatctcttgtacttgaatcatttgggactt ctgcttctgatgctgcactatgctgtcgagctcctctccagcgtgtgcagcctgctttac tttgggggatgagcggtaccagaaagggttgtctttgtggcctatcgtgtttatatccggg tttagtgatgaaaagtaccagaaaggcatatctctgtgggccattgtgtttatcttgggt aatcggaatggaaatgctctctggtaatgtcaatgttggcagctaaaatcgctgtt ctgtcctcgagttgcagtatccaggtgtacataacatggaccttgacgaccgtctggctt cagagatggttagaagatgcgaatcttcatgtctgtgggaggaa------gaga 841 641 181 241 301 880 421 940 0001 1060 1120 1240 1297 121 200 160 820 601 661 1180 721 781 1357 901 1417 원 ŏ g ò g οy g ò qq Qγ d ٥y g ò Q ò Q ò g δ qq ŏ qq οy g ò qq g δ

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diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antisathmatic; antirheumatic; antibarthritic; antiviral; antilinflammatory; antithyroid; antiallergic; antibarthritic; antiviral; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -
                                                                       cancer associated gene; cancer antigen; detection;
                                               Human cancer associated gene sequence SEQ ID NO:204
                                                                                                                                                                                                                                                                                                                                                                                                                                           2352pp; English.
                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                          2000WO-US05882
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                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 776-777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention.
                                                                                                                                                                                                                                                                                                                                             Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-587533/55
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                                                                                                                                                                                                                                                                         08-MAR-2000;
                      08-FEB-2001
                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                               12-MAR-1999;
                                                                                                                                                                                                                                                 21-SEP-2000
                                                                                                                                                                                                                                                                                                                                             Rosen CA,
AAC77810;
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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidibbetic; antiasthmatic; antialrewatic; antiarthritic; antidibbetic; antiasthmatic; antiallergic; antiarthritic; antidioperic; antiasthmatic; antiallergic; antiarthritic; cagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, acardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of

Sequence 2833 BP; 888 A; 504 C; 506 G; 931 T; 4 other;

Length 2833;

12; gtcggcagcggctgcgaccctgggcggcagacgggcggggatggggagcccggcgctggg 409 ggctgcagcggggccgtgaggagcagccagcgggaggcggcggcgagtcggtgagcagct 104 Gaps 73; Indels 650; Score 532; DB 21; Pred. No. 9.2e-94; 0; Mismatches 23.0%; 60.7%; Conservative Similarity Best Local Sim: Matches 1115; Query Match Best Local S 350 45 410 В ă δ

ageggegeagtgateageggtggeggeeggtgagtaceggtgagtacegeggeatgggge 469

atgagoggtaccagaaagggttgtctttgtggcctatcgtgtttatatccgggagactcg 1246 --aatccaaatagaa 1516 ttcagatgaaatttttctacatctcacagttggcttactggtttcatagtttcccggagc 1006 tctacttccagaaagtcaggaaacaagatatcccgggtcaactcatctacattggcctcc 1066 acctetteceacattggaggggeetatetettgtaettgaaccacetgggeetgetgette 1126 tgatgctgcactatgctgtcgagctcctccagcgtgtgcagcctgctttactttgggg 1186 1005 agctggatttcagtactggaaacttcaatgtgttagctgttagaatcgctgttctggcat 1064 cgagttgcagtatccaggtgtacataacatggaccttgacgaccgtctggcttcagagat 1423 ccatttgcgttactcaggcatttatgatgtgtggaagttcattaattttcagcttcgaaggt 1124 284 206 991 826 886 404 464 584 524 885 atgaaaagtatcagaaaggattttctctgtggggcagttctttttgttttgggaagacttc 944 ttegcaagaaaagcaccaagagcececcagtgetgagecacgaattegteetgeagaate acgcggatatggtctcctgcgtgggcatgttcttcgtgctgctgggacttatgttcgagggca aaaactacatctcagacccaactatcttatggagggcttatccccataacctgatgacat atggaaatgctctctctggtaatgtcaatgtgttggcagctaaaatcgctgttctgtcct tecgeaagaagaaegeeaggaaeeeeeggtgetgageeaegaatteatggtgeagaaee cggccgagatgtcgatcgtgttcctcaccctgcagcatggagtcgttgtcccag---cgg eggcaaaagcttctatcattttgttactcttcagtacaatgtcaccctcccagcaacag aagggctaccctcggggtccaggaccctttaccattatggggtcaaagatctggccacag tgttcttctacatgctggtggccatcatcattcacgccaccattcaggagtacgtgctag ataagetcagecggagaetgeagetcaceaaaggeaaacaaaaetgaatgaggeeg ggcagctgagtgtgttctacatagtgtctggtatctggggtatgatcattctggcctctg agaactgcctgtcagaccccactctattgtggaagtctcagccccacaacatgatgacat tgacactgattgtctcagtggttacagtagggcttcacttggccgggac---aaaatcgga ggttagaagatgcgaatcttcatgtcggggaggaagagacggtccagg------= = - tcgagaaaaggcacagaaatggagtggag---585 645 165 945 1065 165 225 590 345 405 465 525 1007 1067 825 470 530 285 647 707 167 827 887 947 705 1127 1187 1364 1304 1424 1125 1474 Qγ d Q g ŏ 9 Qγ g οy g ò qq à g δ g ò g ŏ g Qγ d δ g ò g δ d δ ВÞ ð g g Óγ ò

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                   tagattetecaccaaagaaagaaagaaage-teettageagttgeaagegaattgatte 1575
                                                         ttacctccaagggaatccacttcttcttatgtggtgtctctgtgctagagattttctgtt 1635
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                            1305 atgtccccaaagaaatctgctttctactatatctttcagcattagagatttttctgttct
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                                                                                                                                                                                                                                     The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The CDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynuclectide sequences. The proteins are useful for identifying compounds that modulate their activity and production, and the cell is also useful for identifying compounds that modulate expression of the polynuclectide sequences encoding the secreted proteins. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders
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         Resnick RJ;
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         SH,
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                                                                                                                        New polynucleotides encoding secreted proteins useful asthma, HIV and Crohn's disease
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         Howes
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ed. No. 5.1e-91;
Mismatches 652;
       Agostino MJ,
                                                                                                                                                                                              Claim 1; Page 103-104; 391pp; English.
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ark HF, Fechtel K,
Graham JR;
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         Clark HF,
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                          Gulukota K,
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                          New human transposition chain related membrane protein and its coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translocating chain-associated membrane protein; BioTRAM; ss.
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aaggttaaaactcaaatcagtattatgtaaccgttgggatttttttaaagtgttttaaatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA; 1517
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64.6%;
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New nucleic acid expressed at high level in normal prostatic tissue and encoded polypeptides, used to treat cancer and screen for therapeutic agents 2054 1483 2114 1367 2174 treatment; gene therapy; Rosenthal A; tgcaggataaagtggaaaatctgataaaggttaaactcaaatcagtattatgtaaccgtt aaaaacacagtactaatgggtaacacatatggaggtttgctgccatatattgcatcaa aatatggtggttactaaagaagtaaacgacttcttcctgtttattttaaacacttgtac aatatcattaattaatataaaaatattaaaatcattcctgtccattc----cacttgtaa gggatttttttaaagtgttttaaatttacaatggaaagcatttgtcaaaccacca-aaaa atatgaatagatgacatgtgtggtgatattgacatttagcgaatcaagatacctttaata ы́ Dahl ú tumor; Schmitt A, Pilarsky Expressed sequence tag; EST; prostate; cancer; tissue specificity; human; ss. (META-) METAGEN GES GENOMFORSCHUNG MBH EST Human prostate cancer-associated BP CDNA; 1120 Claim 3; 117; 194pp; German. 98DE-1011194 98DE-1011194 entry) В, 1999-519629/44. Specht T, Hinzmann (first standard; P-PSDB; AAY48434. DE19811194-A1 sapiens 10-MAR-1998; 10-MAR-1998; 16-SEP-1999 AAZ33531 AAZ33531 RESULT 11 1936 2055 1316 2115 1368 2175 1428 Ношо 1198 1996 1256 THE STATE OF THE S g Q g δ Q δ Q QΥ g ò 9

This invention describes novel nucleic acid sequences (A) that are expressed at high level in normal prostatic tissue. Polypeptides (I) perioded by (A) are used: (a) for identifying agents for treatment of prostatic cancer and (b) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate (II)-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTS (expressed sequence tags) before these are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTS. AZ33477-Z33540 represent expressed sequence tags described in the method of the

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The invention relates to primers for synthesising full length cDNA clones, 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention.
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                            synthesizing full length cDNA clones and their
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K, Kojima S, Otsuki
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su A, Sugiyama T, Nagai
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11-JAN-2000; 2000JP-0118774.
02-MAX-2000; 2000JP-0183765.
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                                                                                                                                                                                                                                                                                                       AAK91674 standard; cDNA;
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T, Koga
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K, Kojima
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Wakamatsu A, Sugiyama T, Nagai
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The invention relates to primers for synthesising full length CDNA clones. 830 CDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the CDNA molecules have been determined. Primers for synthesising the full length colona are useful for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length colona without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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6.2e-63;
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Pred. No. 6.2e-
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Human; ss; breast cancer protein; tumour; cancer; cytostatic;
  Human breast cancer cDNA clone 21093
                    WO200179286-A2.
          gene therapy.
               Homo sapiens
                          25-OCT-2001
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17-APR-2000; 2000US-0551621. 08-JUN-2000; 2000US-0590751. 22-JUN-2000; 2000US-0604287. 20-JUL-2000; 2000US-0620405. 12-APR-2001; 2001WO-US12164

Mitcham JL, Jiang Y, Dillon DC, (CORI-) CORIXA CORP.

Hepler WT;

Harlocker SL,

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useful for the prevention, Breast Tumour Proteins and nucleic acids diagnosis and treatment of breast cancer WPI; 2001-611721/70.

Claim 37; Page 266; 297pp; English.

nucleic acids that encode them, including immunogenic fragments of the proteins. Also included are expression vectors expressing the proteins. Also included are expression vectors expressing the proteins. Also included are expression vectors expressing the proteins or an antigen presenting cell expressing the protein. The proteins and concluded are acids may be used in the prevention, diagnosis and treatment of diseases associated with imappropriate breast tumour protein expression, i.e. breast tumours and breast cancer e.g by gene therapy. The nucleic acids and their complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The proteins, nucleic acids and antibodies may be used to dentify modulators (e.g. antagonists) of breast tumour protein acids in assays to dentify modulators (e.g. antagonists) of breast tumour protein and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The antibodies may also be used a diagnostic agents for detecting the presence of the proteins in other ammuno-purification diagnostic techniques. The present sequence is a mundor-purification diagnostic techniques. The present sequence is a considerative. The invention relates to isolated breast tumour proteins and nucleic acids that encode them, including immunogenic fragmen hybridisation against a normal breast cDNA library

Sequence 642 BP; 226 A; 106 C; 141 G; 169 T; 0 other;

641 cagoggaagggctaccctoggggtccaggaccctttaccattatggggtcaaagatctgg 700 625 CAACAGAAGAACAAGCTACTGAATCAGTGTCCCTTTATTACTATGGCATCAAAGATTTG 566 ccacagtgttcttctacatgctggtggccatcatcattcacgccaccattcaggagtacg 760 505 TGTTGGATAAAATTAACAGGCGAATGCACTTCTCCAAAACAAAACACAGCAAGTTTAATG 446 aggocoggocagotgagtgttctacatagtgtctggtatctggggtatgatcattctgg 880 Gaps ; 0 Length 642; 0; Mismatches 175; Indels Score 345; DB 22; Pred. No. 1.1e-57; = 14.9%; 72.0%; Best\_Local Similarity 72.0 Matches 450; Conservative Query Match 565 ( 761 701 445 821 Ω q ò δ QQ Qγ

1060 1180 1240 1000 26 385 TCTCTGAAAACTACATCTCAGACCCAACTATCTTATGGAGGGCTTATCCCCATAACCTGA tgacatttcagatgaaatttttctacatctcacagttggcttactggtttcatagtttcc tgettetgatgetgeactatgetgtegageteeteteeagegtgtgeageetgetttaet 145 ITCTTCTGGTGCTACATTATTTTGTTGAATTTCTTTTCCACATTTCCCGCCTGTTTTATT 881 cctctgagaactgcctgtcagaccccactctattgtggaagtctcagccccacaacatga 1121 941 1061 1241 qq ò g ŏ g οy g δλ 엄 ò QQ ò

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AAF17959/c ID AAF17959 standard; cDNA; 642

BP.

(first entry) 13-MAR-2001 

AAF17959;

cancer associated 21093 coding sequence. Human breast Human; breast cancer associated gene; vaccine; diagnosis; therapy; ss.

WO200060076-A2 Homo sapiens

12-OCT-2000

2000WO-US05308 15-FEB-2000;

99US-0339338. 99US-0389681. 99US-0285480 99US-0433826 23-JUN-1999; 02-SEP-1999; 02-APR-1999; 03-NOV-1999;

(CORI-) CORIXA CORP.

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Harlocker SL; ٦, x JĽ, Mitcham Yuqiu J, Dillon DC,

WPI; 2001-122627/13.

treatment and diagnosis of least an immunogenic portion of An isolated polypeptide useful for the tumors e.g. breast cancer comprises at a breast tumor protein -

Claim 66; Page 220; 238pp; English.

The present invention provides the coding sequences and some protein sequences of proteins associated with breast cancer in humans. These sequences can be used in the diagnosis and treatment of cancers, particularly breast tumours.

Sequence 642 BP; 226 A; 106 C; 141 G; 169 T; 0 other;

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                                                             881 cctctgagaactgcctgtcagaccccactctattgtggaagtctcagccccacacatga 940
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14.9%; Score 345; DB 22; ilarity 72.0%; Pred. No. 1.1e-57; Conservative 0; Mismatches 175;
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Patent No. 5876995
GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LÓCATION: 115...702
OTHER INFORMATION: apoaequorin-encoding gene
 US-09-182-816-24
US-09-471-528-22
US-09-471-528-24
US-09-634-530-24
US-09-634-530-24
US-09-341-568-1
US-08-341-568-1
US-08-911-020-1
US-08-911-020-1
US-08-911-020-1
US-08-911-020-1
US-08-911-020-1
US-08-91-031-9
US-08-461-811-9
US-08-461-811-9
US-08-461-411-9
US-08-461-411-9
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OSCHWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,046A
FILING DATE: 11-25-96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,274
FILING DATE: 02-06-96
ATTORNEY, FAGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6680-105B
TELECOMMUNICATION:
TELEPHONE: 619-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEE: Brown, Martin,
1: 1660 Union Street
San Diego
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TYPE: nucleic acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Sequence 10, Appl
Sequence 11, Appli
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Sequence 11, Appli
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-135-988-5
US-08-135-988-5
US-08-597-2748-5
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US-08-545-1968-10
US-08-545-1968-12
US-09-817-180-1
US-09-027-137-2
US-08-245-1964-63
US-08-242-63-14
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US-08-157-101A-4
US-09-182-816-22
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CLASSIFICATION:
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ORIGINAL SOURCE:
FEATURE:
                                                                    HYPOTHETICAL: NAMI-SENSE: NO
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ZIP: 92037
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VOLUME:
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STATE:
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                                                                                                                                                                       Length 958;
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09447208
Patent No. 6113886
GENERAL INFORMATION:
APPLICAMT: Bryan, Bruce
TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & MCAUliffe
STREET: 4250 Executive Square, 7th Floor
                                                                                                                                                                  Score 67; DB 2; Pred. No. 4.6e-07; 0; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: Heller Ehrman White & McAuliffe
: 4250 Executive Square, 7th Floor
La Jolla
                                                                             DATE: (1985)
DOCUMENT NUMBER: PATENT NO.: 5,093,240
                               Proc. Natl. Acad. Sci. U.S.A
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/447,208
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 0909/135,988
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
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ER: 24727-105C
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FILING DATE: 11-25-96
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APPLICATION NUMBER: 08/597,274
FILING DATE: 02-06-96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,775
REFERENCE/DOCKET NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                  Query Match 2.9%;
Best Local Similarity 63.2%;
Matches 103; Conservative
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COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 619-450-8400
TELEFAX: 619-450-8499
                 Inouye et al
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PUBLICATION INFORMATION:
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COMPUTER READABLE FORM:
                                                                 PAGES: 3154-3158
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                               JOURNAL:
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Patent No. 6152358
CENERAL INFORMATION:
APPLICANT: Bryan, Bruce
TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & MCAuliffe
STREET: 4250 Executive Square, 7th Floor
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OTHER INFORMATION: apoaequorin-encoding gene
PUBLICATION INFORMATION: PATENT NO.: 5,093,240
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Pred. No. 4.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Proc. Natl. Acad. Sci. U.S.A.
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FILING DATE:
CLASSITION TOWNER: US/09/135.4
CLASSITION
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REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.9%;
                                                                                                                                                                                  NAME/KEY: Coding Sequence LOCATION: 115...702
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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APPLICATION NUMBER: 08/55
FILING DATE: 02-06-96
ATTORNEY/AGENT INFORMATION:
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 103; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06
FILING DATE: 11-25-96
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AUTHORS: Incuye, S.
TITLE: Cloning and sequence analysis of cDNA for the luminescent protein JOURNAL: Proc. Natl. Acad. Sci. USA VOLUME: 82(10)
PAGES: 3154-3158
DATE: 1985-05
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APPLICANT: Bryan, Bruce
TITLE OF INVANION: BIOLUMINESCENT NOVELTY ITEMS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                     Query Match 2.9%; Score 67; DB 4;
Best Local Similarity 63.2%; Pred. No. 4.6e-07;
Matches 103; Conservative 0; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Brown, Martin, Haller & McClain
STRRET: 1660 Union Street
CITY: San Diego
                    OTHER INFORMATION: Apoaequorin-encoding gene PUBLICATION INFORMATION:
PATENT DOCUMENT NUMBER: 5,093,240
PATENT FILING DATE: 1987-10-08
PUBLICATION DATE: 1992-03-03
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6680-105
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597, 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08597274A Patent No. 6247995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6680
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
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SEQUENCE CHARACTERISTICS:
LENGTH: 958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02/06/96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 92101-2926
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-597-274A-5
                                                                                                                                                                                                                                                                                       US-09-277-716-5
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APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: SZENT-GYORGYI, CHRISTOPHER CHRISTIAN CHRIST SENCODING THE
CURRENT APPLICATION NUMBER: US/09/277,716A
CURRENT FILING DATE: 1999-103-26
EARLIER APPLICATION NUMBER: 60/102,939
EARLIER FILING DATE: 1998-10-01
EARLIER FILING DATE: 1998-00-15
EARLIER FILING DATE: 1998-00-15
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-03-27
SOFTWARE FILING DATE: 1998-03-27
SOFTWARE FILING DATE: 1998-03-27
SOFTWARE FILING DATE: 1998-03-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Coding Sequence
LOCATION: 115...702
O'TÉR INFORMATION: apoaequorin-encoding gene
PUBLICATION INFORMATION: PATENT NO.: 5,093,240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inouye et al.
Proc. Natl. Acad. Sci. U.S.A.
82
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  24727-105C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-277-716-5; Sequence 5, Application US/09277716A; Patent No. 6232107; Batent No. 6332107;
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION
TELEPHONE: 619-450-8400
                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                             TELEFAX: 619-450-8499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (115)..(702)
                                                                                                                                                                                                                   TOPOLOGY: linear
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FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                              HYPOTHETICAL:
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2083 gttagtgcttacgccccattaaagcatcaaaatatgaatagatgacatgtgtggtgata 2142
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                                                                                                               2203 gacttcttcctgtttattttaaacacttgtacaggaaaactcgcaaaattaaatattact 2262
                                                                                          2143 ttgacatttagcgaatcaagatacctttaataaatatggtgggttactaaagaagtaaaac
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Matches 94; Conservative
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COUNTRY: USA
ZIP: 22040-0747
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Pred. No. 2.8e-06;
0; Mismatches 178; Indels 0
                                                                                                                                                                                                                                                                                                                                                                 Length 958;
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                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 4.6e-07;
                                                                                                                                                                                                                                                                                                                                                               Score 67; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 64, Application US/08821994A
Patent No. 6228643
GENERAL INFORMATION:
APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Diddier RP
APPLICANT: Thomas, Diddier RP
APPLICANT: Depson, lan
TILLE OF INVENTION: Promoters
FILE REFERENCE: PPD 50108
CURRENT APPLICATION WUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-22
BARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
MUMBER OF SEQ ID NOS: 89
                                                                                                                                               LOCATION: 115...702
OTHER INFORMATION: apoaequorin-encodin PUBLICATION INFORMATION:
DOCUMENT NUMBER: 5,093,240
AUTHORS: Inouye et al.
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                             2.9%;
                                                                                                                            NAME/KEY: Coding Sequence LOCATION: 115...702
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Best Local Similarity 49.0
Matches 171; Conservative
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US-08-821-994-64
TOPOLOGY: linear
MOLECULE TYPE: CDNP
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                    PAGES: 3154-3158
DATE: (1985)
                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                    ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 64
LENGTH: 1474
                                                                                                                                                                                                                                                                                                            US-08-597-274A-5
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                                                                                                                                                                                                                                                         VOLUME:
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2168 tttaataaatatggtgggttactaaagaagtaaacgacttcttcctgtttattttaaaca 2227
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APPLICANT: MUNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
Score 64; DB 3; Length 1582;
Pred. No. 3.2e-06;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARGAL SETLICATION NUMBER: US/08/545,196B
FILING DATE: 19-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 205-8000
                                                                                                                                                                                    Sequence 10, Application US/08545196B Patent No. 6080577 GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36.749
REFERENCE/POCKET NUMBER: PF'
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TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-840 ... INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: FINGTH: 2852 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11ne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94304
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APPLICANT: GAN, Weiniu et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MELKI, JUDITH
APPLICANT: MUNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.8%; Score 64; DB 3; Length 1582; Best Local Similarity 65.3%; Pred. No. 3.2e-06; Matches 94; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                COUNTEY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIOW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B
FILING DATE: 19-OCT-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 32,350
REFERENCE/POCKET NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELEFONE: (703) 205-8000
TELEFAX: (703) 205-8050
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                  1556 AAAAAAAAAAAAAAAAAAAAAAA 1579
                                                                                                RESULT 8
US-08-545-1968-12
Sequence 12, Application US/08545196B
Patent No. 6080577
GENERAL INFORMATION:
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US-08-545-196B-12
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US-09-817-180-1
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2191 aaagaagtaaacgacttcttcctgtttattttaaacacttgtacaggaaaactcgcaaaa 2250
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                                                                                                                                                                                                                                                                                                            Query Match 2.7%; Score 63.4; DB 4; Length 2674; Best Local Similarity 70.2%; Pred. No. 6e-06; Matches 85; Conservative 0; Mismatches 36; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER TEACHBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,137
FILING DATE: Filed Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Vue, Henry
TITLE OF INVENTION: CAFI-RELATED PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: Palo Alto
CITY: Palo Alto
; TITLE OF INVENTION: THEREOF;
; FILE REPERENCE: CLOOLIB3
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARRE: FRASEO for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Human
; USGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF-0476 US
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US-08-909-965C-8
                                                                                                                 Query Match
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FEATURE:
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                                                                              Length 2852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09721822A
Patent No. 6306606
GENERAL INFORMATION:
APPLICANT: MICHAEL J. Weber
APPLICANT: Jacqueline Wyatt
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTIESENSE MODULATION OF MP-1 EXPRESSION
FILE REFERENCE: RTS-0142
CURRENT FILLING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 135
                                                                                                                Indels
                                                                               Score 63.4; DB 3;
Pred. No. 6.2e-06;
0; Mismatches 21;
                                                                                                                                                                                                                                  Sequence 63, Application US/08821994A

Sequence 63, Application US/08821994A

Patent No. 6228643

GENERAL INFORMATION:
APPLICANT: Thomas, Didier RP
APPLICANT: Thomas, Didier RP
APPLICANT: Jepson, Ian
TITLE OF INVENTION: Promoters
FILE REFERENCE: PPD 50108

CURRENT APPLICATION NUMBER: US/08/821,994A

CURRENT APPLICATION NUMBER: PCT/GB97/00729

EARLIER APPLICATION NUMBER: GB 9606062.9

EARLIER FILING DATE: 1997-03-18

EARLIER FILING DATE: 1996-03-22

NUMBER OF SEQ 1D NOS: 89

SOFTWARE: PatentIn Ver. 2.1
                                                                                 2.78;
78.48;
                                                                          Query Match
Best Local Similarity 78.4<sup>§</sup>
Matches 76, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 71.6
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Brassica napus
US-08-821-994-63
   PROSNOT16
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; LIBRARY: PROSN(
; CLONE: 2229466
US-09-027-137-2
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LENGTH: 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1441
                                                                                                                                                                                                                                                                                                              US-08-821-994-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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COUNTRY: U.S.A.
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/909,965C
FILING DATE: August 12, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: FITZPATRICK, CELLA, HARPER AND SCINTO STREET: 277 Park Avenue CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL DNA, NOVEL PUTITLE OF INVENTION: AND NOVEL ANTIBODY NUMBER OF INVENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DIMBER: 97 32745/95
APPLICATION NUMBER: PCT/JP96/03630
FILING DATE: 12-No. 5936078-1995
FILING DATE: 12-Dec-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08909965C
Patent No. 5936078
GENERAL INFORMATION:
APPLICANT: Ruga Tetsro
APPLICANT: Nakagawa Satoshi
APPLICANT: Sakaki yoshiyuki
APPLICANT: Labaki Applicant: Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-2400
TELEPAX: 212-758-2982
TELEXX: 322-758-2982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
ORIGINAL SOURCE:
ORGANISM: human
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-758-2982
TELEX: 236.262
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 1512 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lawrence S. Perry REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 78.9
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (147)...(521)
; OTHER INFORMATION:
US-09-721-822A-10
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STRANDEDNESS:
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2110 tcaaaatatgaatagatgacatgtgtggtgatattgacatttagcgaatcaagatacctt 2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2140 TGAAAGTCTAAATAATGCTGTATAGATATGTATATGGTTCACATATCTGGATCTGTG 2199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Racie, Lisa A.
APPLICANT: Preacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ACCOUNG THEM
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 62.8; DB 2; Length 2
Pred. No. 8e-06;
0; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/014,969 FILING DATE:
                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09014969
Patent No. 5965397
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 496-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.7%;
Best Local Similarity 56.9%;
Matches 115; Conservative
                                                                                                                                                                                    5159 AAAAAAAAAAAA 5173
                                                                                                                                              2293 aaaaaaaaaaaaa 2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: CDNA US-09-014-969-14
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02140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                     US-09-014-969-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08242677

Sequence 1, Application US/08242677

Sequence 1. Sof7143

GENERAL INFORMATION:
APPLICANT: Gaynor, Richard B
APPLICANT: Wu, Foon W.
TITLE OF INVENTION: Callular Nucleic Acid Binding Protein
TITLE OF INVENTION: and Uses Thereof in regulating Gene Expression and in the TITLE OF INVENTION: 9
CORRESPONDENCE: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: AFROIG White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                  1391 TACCAAATTATTTTCACAAAATTAGAAAAAAATCCAAAAATTCATATGGAACCAAAAA 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2173 taaatatggtgggttactaaagaagtaaacgacttcttcctgtttattttaaacacttgt 2232
                                                                                                                                                                 Length 1512;
                                                                                                                                                                                                         25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45; Indels
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 63; DB 1;
Pred. No. 1.1e-05;
                                                                                                                                                               Score 63; DB 2;
Pred. No. 5.5e-06;
0; Mismatches 25
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                                                                                 by experiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MAYTELEI, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEPHONE: 713-789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
; NAME/KEY: CDS
; LOCATION: 78 to 155
; LOCATION: 618 to 725
; LOCATION: 884 to 1018
; IDENTIFICATION METHOD: US-08-909-965C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 5173 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.7%
Best Local Similarity 66.7%
Matches 90; Conservative
                                                                                                                                                                                                       78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-242-677-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-242-677-1
                                                                                                                                                                 Query Match
                                                                                                                                                                                                    Matches
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Search completed: September 6, 2002, 15:16:46 Job time: 7710 sec

BM045930 603624955 BIB30439 603073495 BIB30439 603073495 BM459490 AGENCORT A1848290 UI-M-AHI-BG547017 603573813 BG714759 602673813 BG714759 602673845 A1128453 AU128453 BG77352 H3014E03-BG975574 602845246 BG975574 602845246 BG714581 602671468 BG71458 601165579 BF984410 602307936 BF984410 602307936 BG614318 602642420 BM486565 59710-ph0

AI201635 qb81d09.x

OM nucleic

Run on:

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603351703F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5359105 5', mRNA sequence.
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// Organism=*Mus musculus"
// Organism=*Mus musculus"
// Organism=*Mus musculus"
// Organism=*Mus musculus"
// Organism=*Nusulus
// Organism=*Nusulu
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S NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
Unpublished (1999)

C Ontact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov Laboratory
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
Plate: LLAM1913 row: f column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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Location/Qualifiers
                                                                                             A1848290
BG547017
B1733351
BG714759
AU128453
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BF984410
BF141338
BG614318
BM486565
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BM459490
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DEFINITION
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BB641088 BB641088
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BB62449 BB662449
BB109193 UT.R.BS1-
BE109193 UT.R.BS1-
BC020283 Homo sapi
AL523342 AL523342
BM66240 AGENCOURT
                                                                                                            ; Search time 3580.18 Seconds
(without alignments)
8712.261 Million cell updates/sec
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                                                                                                                                                                                                             Description
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                           13736207 segs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                       Potal number of hits satisfying chosen parameters:
                                                                                                              6, 2002, 00:11:01
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Listing first 45 summaries
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    nucleic search, using sw model

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/organism="Mus musculus"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone='Indage:5359106"
/clone=lib="NIH_MGC_94"
/tissue_type="retina"
/tissue_type=
                                                                                                                                           NIH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM1913 row: f column: 03
High quality sequence stop: 773.
Location/Qualifiers
CCE
                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus

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                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 773)
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Pred. No. 4.4e-82;
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93.6%;
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Matches 771; Conservative
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L. Ontact: Yoshihide Hayashizaki, Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-9226
Fax: 81-45-503-9216
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URL: http://genome.ggs.criken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rappid discovery of new
penes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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agtctcagccccacaacatgatgacatttcagatgaaatttttctacatctcacagttgg
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SAGAGAGAGATTCCCCCCCCCC 3']. CDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                  contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                       /clone_lib-"RIKEN full-length enriched, 16 days embryo head"
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                                                                                                                                                                                                                                                    /tissue_type="head"
/dev_stage="16 days embryo"
/lab_host="DH10B"
                                                                                                       /ordanism="Mus musculus"
                                                                                                                                          /db_xref="taxon:10090"
/clone="C130035P06"
                                                           Location/Qualifiers
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                                                                                                                             /strain="C57BL/6
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RESULT LOCUS ORGANISM

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE ACCESSION

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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A830091N21"
/clone_lib="RIKEN full-length enriched, 10 days neonate
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                                                                                                      /tissue_type="cortex"
/dev_stage="10 days neonate"
/lab_host="DH10B"
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishil, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Saaki, C., Sano, H., Sasaki, D., Shibata, K., Sinnagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

FIREN Mouse ESTS (Arakawa, T., et al. 2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 26-OCT-2001
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Normalization and subtraction of cap-trapper-selected cDNas to prepare full-length cDNa libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Calcuratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tai: 81-45-503-9216
Fax: 81-45-503-9216
Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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                                                                                                                         1018
                                                                                                                                                                                                                                                                                                                                      BB641088 FIKEN full-length enriched, 10 days neonate cortex Mus musculus cDNA clone A830091N21 5', mRNA sequence.
                                                                                                                                                             629
                                          480 TGTTCTATATAGTGTCCGGGATCTGGGGCATGATCATTCTGGCCTCTGAGAACTGCCTGT
                                                                                                                       ttttctacatctcacagttggcttactggtttcatagtttcccggagctctacttccaga
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TITLE JOURNAL COMMENT

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601 AGGCACAGAAATGGAGTGGAGAATCCGAATAGAATAGACTCTCC 645
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomuras, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahsshi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, T., et al. 2001)

L. Unpublished (2001)

On Jul 28, 2000 this sequence version replaced gi:9572973.
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Fax: 81-45-503-9226
Email: genome-resegac.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
W., Konno,H., Okazaki,Y., Muramatsu,M. and Hayshizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full:length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayshizaki,Y.
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10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashiazki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinaqawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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/organism="Mus musculus"
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/clone="D930001M01"
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Location/Qualifiers
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Hayashizaki,Y.
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                                                                                                                                      RESULT
BB521515
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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                                                               prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 942 gacatttcagatgaaatttttctacatctcacagttggcttactggtttcatagtttccc 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Site_1: SalI; Site_2: BamHI; cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                            645;
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Pred. No. 1.9e-66;
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/tissue_type="head"
/dev_stage="15 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                          174
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95.0%;
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DEFINITION

ACCESSION

VERSION KEYWORDS

RESULT BB662449

ORGANISM

SOURCE

AUTHORS

REFERENCE

TITLE JOURNAL

COMMENT

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G10 bp mRNA linear EST 13-JUN-2000 UI-R-BS1-azd-a-04-0-UI.S1 UI-R-BS1 Rattus norvegicus CDNA clone UI-R-BS1-azd-a-04-0-UI 3', mRNA sequence. BE109193. G1:8501298 EST.
                                                                                      was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
              contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGAGAGACTCTTTTTTTTTTTTTTVN 3'], cDNA was
RIKEN. Division of Experimental Animal Research in Riken
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                                                                                                                                                                                                                                                                                                                                                                                  Length 628;
                                                                                                                                                                                                                                                                                                                                                                               Score 587; DB 9;
Pred. No. 1.7e-65;
0; Mismatches 25;
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                 l (bases 1 to 628)
Arakava,T., Carninoi,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
Alakava,T., Carninoi,P., Fukuda,S., Furuno,M., Rawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
Unpublished (2001)
                                                                        BB662449 RIKEN full-length enriched, 15 days embryo head Mus musculus CDNA clone D930001M01 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URL: http://genome.resegsc.riken.go.jp,
URL: http://genome.go.pr,
URL: http://genome.go.pr,
Carninci.p., Shibata,Y., Hayasu.N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Huramatsu,M. and Hayashizaki,Y.
N., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length.cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
Laboratorry for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/dev_stage="15 days embryo"
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/organism="Mus musculus"
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/clone="D930001M01"
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FEATURES

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Query Match
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KEYWORDS
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BI985062
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/dev_stage="embryonic 13 dpc"
/lab_host="bH10B (Life Techhologies)"
/lab_host="bH10B (Life Techhologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BS1
library is derived from 13 dpc whole embryo tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
ratestr.eng ulowa.edu.
TAG_LIB-UI-R-BS1
TAG_TISSUE-embryo at 13 dpc
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                                                                                                                                                                                                                                                                             Email: mosares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized embryo at 13 dpc library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                Bonaldo,M.F., Lennón,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UT-R-BS1-azd'a-04-0-UI"
/clone_llb="UT-R-BS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.0%; Score 577.6; DB 9 98.3%; Pred. No. 2.6e-64; iive 0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
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                                                                                                                                           Genome Res. 6 (9), 791-806 (1996)
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600 bp mRNA linear EST 20-DEC-2001
3131-07 Mouse E14.5 retina lambda 2AP II Library Mus musculus CDNA,
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu,X., Zhao,S., Pershad,R., Hsleh,T.-F., Scarpa,A., Wang,S.W., White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
Gene expression in the developing mouse retina by EST sequencing and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
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ggtgatgactgcagaattgtgtacataaataatagtttcctgcttccaatgttctttatc 1887
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/tissue_type="neural retina"
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159 c 168 g 140 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Fat: 713 790 0329.
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Pred. No. 7.8e-59;
0; Mismatches 26; ]
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Pred. No. 6.6e-54;
0; Mismatches 410;
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clone has the following problem:
    Location/Qualifiers
                                                                                                                                   : pCMV-SPORT6"
268 q 408 t
                           1. .1356
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4519858"
/tissue_type="Prostate, a /clone_lib="NIH_MGC_91"
/lab_host="DH108"
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                                                                                                                                     /note="Vector:
                                                                                                                                                                                                            21.4%;
65.0%;
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Best Local Similarity
Matches 825; Conserv
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Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Parayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing Center
Center code: BECM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm .tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M.,Holloway, M., Talford, B. Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gunarathe, P., Yoon, V., Kowis, C., Martin, R.,
Lawrence, S., Richards, S., Gibbs, R.A.
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Submitted (20-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg, R.
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Homo sapiens, clone IMAGE:4519858, mRNA.
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human.

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

LOCUS

RESULT BC020283

USA

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REFERENCE AUTHORS TITLE JOURNAL

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1064)
Li,W.B., Gruber.C., Jessee,J. and Polayes,D.
Full.length cDNA libraries and normalization
Unpublished (2001)
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BP 191 9106 EVRY cedex - France
Emall: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                              889 GITGGTTTTGGCCTTGCAAGAGCAGAAATCAGAAGCTGGATTTCAGTACTGGAAACTTC
                                                                                 aatgigitgicagciaaaaicgcigitcigiccicgagitgcagiaiccaggigiacaia
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/lab_host="DH108"
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/db_xref="taxon:9606"
/clone="CSODCO011H18"
/clone_lib="ITI_NFL003_NBC3"
/sex="male"
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VERSION
KEYWORDS
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Pred. No. 1.6e-52;
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                                                                                                                   1142 bp mRNA linear EST 05-FEB-2002 1. mRNA sequence.

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/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library. 3 others
1 282 c 233 g 341 t 3 others
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                                                                                                                                                                                                                                                                BM466240.1 GI:18515282
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622 bp DNA linear GSS 27-APR-2001
2M0226CO6R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
610ne UUGC2M0226CO6 R, DNA sequence.
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                  973 cagtiggettactggtttcatagtttcccggagetctacttccagaaagtcaggaaacaa 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 ATTATTCATGCCGTAATTCAAGAGTATATGTTGGATAAAATTAACAGGGGAATGCACTTC 384
                                                                                                                                                                                                   445 GCCTGTGTTTGGGGCACATTCATTCTCATCTTGAAAACTACATCTCAGACCAACTATC 504
                                                                                                                                                                                                                                                                            685 CITITGAACTIGAATCATCIAGGACTIGITCTTCTGGTGCTACATTATTTTGTTGAATTT 744
                                                                                                                          385 TCCAAAACAAAACACAGCAAGTTTAATGAATCTGGTCAGCTTAGTGCGTTCTACCTTTTT 444
                                                                              793 accaaaggcaaacaaaacaaattgaatgaggccgggcagctgagtgtgttctacatagtg
                                                                                                                                                                                 853 tctggtatctggggtatgatcattctggcctctgagaactgcctgtcagaccccactcta
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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Unpublished (2000)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E. I (bases 1 to 1135)
I (bases 1 to 1135)
I (bases 1 to 1135)
L Unpublished (1999)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue prourement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM12329 row: 1 column: 16
High quality sequence stop: 710.
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Pred. No. 9.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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70.2%;
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    Homo sapiens
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                                                  /Jab.host-EE. coli strain XL10-Gold, T1-resistant, F."
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/G1 (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymorleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114)plARI29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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AGENCOURT_6457038 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5576991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tcctgggaagccctccggctcccgcgggtgggcggcggcggcgatcggtgcggcaaatc 237
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/clone="UUGC2M0226C06"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 418.2; DB 12; Length 622;
Pred. No. 4.2e-44;
0; Mismatches 18; Indels 6;
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                                            /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 18.1%;
Best Local Similarity 95.0%;
Matches 455; Conservative
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BM466239
BM466239.1 GJ.10---
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Isogai, T.

RIN human cDNA project (Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y., Saito, K., Yamamoto, J., Nishikawa, T., Nakamura, Y., Nagai, T., Sugano, S., Masuho, Y., Isogai, T.)

Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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7 5', mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ota.T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
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                                                                                                gatatecegggteaacteatetaeattggeeteeaceteteeacattggagggeetat 1092
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                                                                                                                746 CTTTTCCACATTTTCCGCCTGTTTTATTTTAGCAATGGAAAAGTATCAGAAAGGGATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="teratocarcinoma"/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo saplens"
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/clone_lib="NT2RP4"
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AU132871.1 GI:10993410
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COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 822)
Ota.T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
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                                                                                                                                    436 ccggtgagtaccggtgagtaccggggcatggggctccgcaagaagaacgccaggaacccc 495
                                                                                                                                                                                                                                                                                                ctttaccattatggggtcaaagatctggccacagtgttcttctacatgctggtggccatc 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              618 GATATTCCTCGTCAGCTTGTCTACATTGGTCTTTACCTCTTCCACATTGCTGGAGCTTAC 677
                                    Gaps
                                                                                       1153 ctctccagcgtgtgcagcctgctttactttgggggatgagcggtaccagaaagggttgt 1210
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Score 392.4; DB 9;
Pred. No. 7.5e-41;
                                  0; Mismatches 223;
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17.0%;
70.7%;
                                  Conservative
                  Best Local Similarity
Matches 550; Conserv
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/organism="Homo sapiens"
/do_xref="taxon.9606"
/clone="WT2RP3000388"
/cell_type="teratocarcinoma"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 2 "weeks retinoic acid (RA) induction"
                                                                                                                                                                                                                                                                                                                                  Ή;
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
153-2 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix
Research Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 TTCTTCTGATGCTCCATTATTTTGTTGAATTTCTTTTCCACATTTCCGCCTGTTTTATT 576
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                                                                                                                                                                                                                                                                                                           DB 9; Length 822;
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Pred. No. 8.4e-39;
0; Mismatches 220; Indels
                                                                                                                                                Location/Qualifiers
                                                                                                                                       Helix Research Institute.
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Best Local Similarity 70.0%;
Matches 520; Conservative
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 TITLE
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Search completed: September 6, 2002, 13:07:54 Job time: 46613 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

; Search time 74.4 Seconds
(without alignments)
541.933 Million cell updates/sec 6, 2002, 14:51:51 September Run on:

US-09-807-470-2 1892 1 MGLRKKNARNPPVLSHEFMV......NGVENPNRIDSPPKKKEKAP 363 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 seqs, 111073796 residues Searched:

747574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

1. \SIDSI\gardata\hold-geneseqy\geneseqp-embl\AA1980.DAT:\*
2. \SIDSI\gardata\hold-geneseqy\geneseqp-embl\AA1980.DAT:\*
3. \SIDSI\gardata\hold-geneseqy\geneseqp-embl\AA1981.DAT:\*
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16. \SIDSI\gardata\hold-geneseqy-embl\AA1992.DAT:\*
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18. \SIDSI\gardata\hold-geneseqy-geneseqp-embl\AA1992.DAT:\*
19. \SIDSI\gardata\hold-geneseqy-geneseqp-embl\AA1992.DAT:\*
118. \SIDSI\gardata\hold-geneseqy-geneseqp-embl\AA1992.DAT:\*
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119. \SIDSI\gardata\hold-geneseqy-geneseqp-embl\AA1992.DAT:\*
210. \SIDSI\gardata\hold-geneseqy-geneseqp-embl\AA1992.DAT:\*
211. \SIDSI\gardata\hold-geneseqy-geneseqp-embl\AA1992.DAT:\*
221. \SIDSI\gardata\hold-geneseqy-geneseqp-embl\AA1992.DAT:\*
222. \SIDSI\gardata\hold-geneseqy-geneseqp-embl\AA1992.DAT:\* A\_Geneseq\_032802:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Rat WAR-1 amino ac	Rat WAR-1 protein	Human WAR-1 amino	Novel human diagno	Human WAR-1 protei	Human polypeptide,	Human cancer assoc	Human prostate can	Human reproductive	Drosophila melanod	Drosophila melanog
ΩI	AAY98146	AAB70696	AAY98147	ABG12234	AAB70695	AAM93265	AAB43601	AAY48434	AAM95708	ABB65847	ABB66114
DB	21	22	21	22	22	22	21	20	22	22	22
Length	363	363	369	369	369	369	416	304	384	368	368
Query e Match Length DB I	100.0	100.0	77.3	77.3	77.3	77.3	0.09	48.7	39.1	29.9	29.9
Score	1892	1892	1463	1463	1463	1462	1134.5	922	739	266	266
Result No.	1	7	3	4	S	9	7	80	6	10	11

Endoplasmic reticulum protein WAR-1 which inhibits cancer cell proliferation for use in treatment and diagnosis of cancer including sarcomas of high malignancy

Drosophila melanog Human secreted pro	Saccharomyces cere	protein		Human secreted pro	Human polypeptide	•••	Arabidopsis thalia	Arabidopsis thalia	Novel signal trans	Novel signal trans	Human olfactory re	Human OR-like poly	Human LAPH-2 prote	Human hydrophobic	Human apoptosis pr	Human cancer assoc	Arabidopsis thalia	Human secreted pro	Drosophila melanog	Zea mays protein f	Chlamydia trachoma	Human polypeptide	Novel human diagno	Arabidopsis thalia	Human G protein-co	Human olfactory re	Human olfactory re	Human olfactory re	Human olfactory re	Human olfactory re	G-protein coupled
ABB67362 AAG00189	AAR86810	AAM78909	AAB93884	AAB24489	AAM42028	AAM79893	AAG44196	AAG44197	AAU17576	AAU17201	AAG72224	AAG72549	AAY00877	AAB88560	AAU00782	AAB43806	AAG41779	AAB34938	ABB67693	AAG33404	AAY37316	AAM40417	ABG30056	AAG41780	AAY90877	AAU24525	AAG72073	AAG72203	AAG72870	153	AAU10312
22 21	17	22	22	21	22	22	21	21	22	22	22	22	20	22	22	21	21	21	22	21	20	22	22	21	21	22	22	22	22	22	22
1575 125	394	394	394	191	488	536	296	280	. 158	181	312	312	380	380	311	266	310	150	232	313	397	533	431	254	313	313	313	307	315	324	309
		7.3	7.	7.	9	9	9	9	5.9	•				ۍ 8.	•	9.6	5.6	5.4	5.2	5.2	2.5	5.5	•	5.1	4.9	4.9	4.9	4.8	4.8	4.8	4.8
56 14.	148.5	38.	138.5	133.5	117	117	115.5	114.5	111.5	111.5	111	111	110	110	108	106.5	105.5	101.5	86	97.5	97.5	97.5	96.5	96	93	93	92	91	91	91	90
12	14 15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Endoplasmic reticulum; WAR-1; cancer cell proliferation inhibitor; Ishikawa H; Х, Nemoto Tojo S, AAY98146 standard; Protein; 363 AA Komiya K, diagnosis; cancer; sarcoma; rat. Rat WAR-1 amino acid sequence. (SUMU ) SUMITOMO PHARM CO LID. 98JP-0290711. 99WO-JP05631. (first entry) Tohdoh N, Yoshima T, Okuyama H; WPI; 2000-317980/27. N-PSDB; AAA38012. norvegicus. WO200022123-A1. 13-OCT-1999; 13-OCT-1998; 22-AUG-2000 20-APR-2000 AAY98146; Rattus Н AAY98146 RESULT 

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(SUMU ) SUMITOMO PHARM CO LID.
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                                This sequence represents an endoplasmic reticulum protein (WAR-1) amino acid sequence. The invention includes rat and human WAR-1 sequences, expression vectors containing the DNA, cells transformed with the kypression vector, antibodies against WAR-1, and probes and primers hybridise to the DNA encoding WAR-1. The WAR-1 protein inhibits the proliferation of cancer cells, and is used in the treatment and diagnosis of cancers including highly malignant sarcomas.
                                                                                                                                                                                                             AEGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNE 120
                                                                                                                                                                                                                         AGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSFP 180
                                                                                                                                                                                                                                                              240
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                                                                                                                                                                                                   09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WAR-1; protein screening; endoplasmic reticulum membrane protein; endoplasmic reticulum membrane transportation; secretory protein; cell membrane protein; cytostatic; CNS active; antiallergic; cancer; antirheumatic; nervous system disorder; immune disorder; allergy; rheumatism; skeletal disorder.
                                                                                                                                                                                   ELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLYF
                                                                                                                                                                                                                                                                                                                            GDERYQKGLSLMPIVFISGRLVTLIVSVVTVGLHLAGTNRNGNALSGNVNVLAAKIAVLS
                                                                                                                                                                                                                                                                                                                                       SSCSIQVYITWTLTTVWLORWLEDANLHVCGRKRRSRSRKGTENGVENPNRIDSPPKKKE
                                                                                                                                                             ;
0
                                                                                                                                        DB 21; Length 363;
                                                                                                                                                            Indels
                                                                                                                                      Score 1892; DB 21;
Pred. No. 3.8e-213;
Mismatches 0;
                            This sequence represents an endoplasmic acid sequence. The invention includes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat WAR-1 protein sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB70696 standard; Protein; 363 AA.
           2; 89pp; Japanese.
                                                                                                                                                         0;
                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                        Conservative
                                                                                                                                  Query Match
Best Local Similarity
Matches 363; Conserv
                                                                                                          AA;
          Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200114582-A1.
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          Claim 1;
                                                                                                        Sequence
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The present invention describes a screening method for secretory and membrane proteins consisting of transformation of a cell with separate expression vectors for the sense and antisense RNA of DNA encoding an endoplasmic reticulum membrane protein participating in endoplasmic reticulum transport of proteins. Also described are: (1) secretory and cell membrane proteins identified by the screening method; (2) drug compositions containing these proteins; (3) host cells transformed by the separate expression vectors of the method and (4) the preparation of secretory and cell membrane proteins by culture of the transformants. The method can be used for the identification and preparation of proteins for use in the treatment and prevention of diseases such as cancer, disorders of the nervous system, immune disorders (including lepresents a specifically claimed rat WAR-1 protein from the present
                                                                                                       Transformation of a cell with separate vectors expressing the sense and antisense strands of WAR-1 DNA for screening secretory and membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNNMTFQMKFFYISQLAYWFHSFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 363;
           Nemoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1892; DB 22;
Pred. No. 3.8e-213;
Mismatches 0;
           н,
         Ishikawa
                                                                                                                                                                                    Claim 3; Page 60-62; 79pp; Japanese.
      Imamura M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY98147 standard; Protein; 369 AA.
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Tohdoh N, Okuyama H,
                                      WPI; 2001-202940/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Best Local Simi.
Matches 363; (
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ABG12234 standard; Protein; 369 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -AEGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSSSCSIQVYITWTLTTVWLQRWLEDANLHV-CGRKRRSR-SRKGTEN--GVENPNRIDS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                   Endoplasmic reticulum protein WAR-1 which inhibits cancer cell proliferation for use in treatment and diagnosis of cancer including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGLRKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endoplasmic reticulum; WAR-1; cancer cell proliferation inhibitor;
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                                                                                                                                                                                                            Ishikawa H;
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                                                                                                                                                                                                            Nemoto K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 1463; DB 21;
; Pred. No. 9.6e-163;
43; Mismatches 40;
                                                                                                                                                                                                            Tojo S,
                                     diagnosis; cancer; sarcoma; human.
                                                                                                                                                                                                            Komiya K,
Human WAR-1 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 2; 89pp; Japanese.
                                                                                                                                                                                   (SUMU ) SUMITOMO PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.3%;
75.8%;
                                                                                                                                                          98JP-0290711.
                                                                                                                                                                                                                                                                                                proliferation for use in tre
sarcomas of high malignancy
                                                                                                                                   99WO-JP05631
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                                                                                                                                                                                                           Yoshima T,
                                                                                                                                                                                                                                               WPI; 2000-317980/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 AA;
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                                                                                                                                                                                                                                                            N-PSDB; AAA38013
                                                                                   WO200022123-A1.
                                                             Homo sapiens
                                                                                                                                   13-OCT-1999;
                                                                                                                                                          13-OCT-1998;
                                                                                                           20-APR-2000
                                                                                                                                                                                                                        Okuyama H;
                                                                                                                                                                                                           Cohdoh N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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NAME OF THE PROOF

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

Specification, but was obtained in electronic format directly from WIPO specification of the printed and polynery of the sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                        n; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
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Pred. No. 9.6e-163;
3; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 42593; 103pp; English.
                                                                                                                            Novel human diagnostic protein #12225.
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75.88;
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23-AUG-2000; 2000US-0649167.
                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73
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                                                                                                                                                                                                                                                                                          Homo sapiens
                                                            18-FEB-2002
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Best Local Simi
Matches 279;
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ABG12234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transformation of a cell with separate vectors expressing the sense and antisense strands of WAR-1 DNA for screening secretory and membrane
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                                                                                                                                                 300
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                                                                                                                                                                                        EAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSF 179
                                                                                                                                                                            354
aaeeqatgskslyyygvkdlatvffymlvaiiihatiqeyvldkinkrmqftkakqnkfn 120
                                                                                                                                                                                                                                                                                                                                                                                                              WAR-1; protein screening; endoplasmic reticulum membrane protein; endoplasmic reticulum membrane transportation; secretory protein; cell membrane protein; cytostatic; CNS active; antiallergic; cancer; antitrheumatic; nervous system disorder; immune disorder; allergy; rheumatism; skeletal disorder.
                                    FGDERYQKGLSLWPIVFISGRLVTLIVSVVTVGLHLAGT-NRNGNALSGNVNVLAAKIAV
                                                                                                                                         LSSSCSIQVYITWTLTTVWLQRWLEDANLHV-CGRKRRSR-SRKGTEN--GVENPNRIDS
                                                                          PELYFOKVRKODIPGOLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLY
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                                                                                                                                                                                                                                                                                                                                                                                          Human WAR-1 protein sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 58-60; 79pp; Japanese.
                                                                                                                                                                                                                                                                                                                 AAB70695 standard; Protein; 369 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins expressed by the cell
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N-PSDB; AAF74780, AAF74782.
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                                                                                                                                                                                                                             PPKKKEKA 362
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61
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AAB70695
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cancer, disorders of the nervous system, immune disorders (including allergies and rheumatism) and skeletal disorders. The present sequence represents a specifically claimed human WAR-1 protein from the present
                                                                                                                                                                                                                                                                                                                                                                                                                     61 -AEGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLN 119
                                                                                                                                                                                                      Gaps
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Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                                                                  120 EAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSF
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                                                                                                                                                             Length 369;
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                                                                                                                                                           77.3%; Score 1463; DB 22;
75.8%; Pred. No. 9.6e-163;
iive 43; Mismatches 40;
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K, Kojima
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su A, Sugiyama T, Nagai
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11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
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                                                                                                                                                                                  Best Local Similarity 75.8
Matches 279; Conservative
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N-PSDB; AAK94181.
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                                                                                                      AA;
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                                                               invention.
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neurological disease; drug screening

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                                                                                                                                                    molecules have been determined. Primers for synthesising the full length the CDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched CDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
antlinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -AEGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGLRKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PELYFOKVRKODIPGOLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLY
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                                                                                                                                                                                                                                                                                                                                                                                                       77.3%; Score 1462; DB 22; Length 369; 75.5%; Pred. No. 1.3e-162; 1ive 44; Mismatches 40; Indels 6
                                                            Claim 8; SEQ ID NO 2725; 1380pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cancer associated protein sequence SEQ ID NO:1046.
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|ppkrkeks 368
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Matches 278;
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AAC77607 to AAC7848 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antiallergic; antiarthritic; antinflammatory; antithyroid; antiallergic; antibacterial; antiviral; cerminoflammatory; antipprofective; cardiant; the corroptic; vasotropic; antipprofective; cardiant; the coording and polypeptides can be used for preventing, treating or polynucleotides and polypeptides can be used for preventing, treating or meliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or immune cells, to treat disorders of haematopoletic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate confermation cancers, ardiovascular disorders, nucleotides, antibodies, bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to the confermation of the present sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 A-EGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PELYFOKVRKODIPGOLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGLRKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVP 60
                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acids comprising sequences encoding peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGDERYQKGLSLWPIVFISGRLVTLIVSVVTVGLHLA-GTNRNGNALSGNVNVLAAKIAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 4.5e-124; 61; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                               useful for treating or diagnosing e.g. cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 1634-1636; 2352pp; English.
                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                     08-MAR-2000; 2000WO-US05882.
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                                                                                                                                                                                                                                                                         Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                2000-587533/55.
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Matches 219; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             416 AA;
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                                                                         W0200055350-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid expressed at high level in normal prostatic tissue and encoded polypeptides, used to treat cancer and screen for therapeutic
                                                                                                                                                                                                                                                                                                            Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy; cancer; tissue specificity; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosenthal A;
LSSSCSIQVYITWTLTTVWLQRWLEDANLHVCGRKRR-----SRSRKGTENGVE---NP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 VSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSFPELYFQKVRK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 TLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQLSVFYI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.7%; Score 922; DB 20;
58.1%; Pred. No. 2.5e-99;
tive 48; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                               Human prostate cancer-associated protein 131.
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                                                                                                                                                                              AAY48434 standard; Protein; 304 AA.
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Matches 176; Conservative
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                                                                                               403 nvadsprnkkeks 415
                                                              350 NRIDSPPKKKEKA 362
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N-PSDB; AAZ33531.
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Human; reproductive system related antigen; reproductive system disorder;
241 mmwkfinfqlrrwrehsafqapavkkkptvtkgrsskkgtengvngtltsnvadsprnkk
                                                                                                                                                                                                                 309 ITWTLTTVWLQRWLEDANLHVCGRKRR----SRSRKGTENGVE---NPNRIDSPPKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human reproductive system related antigen SEQ ID NO: 4366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM95708 standard; Protein; 384 AA.
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2000US-0189874
2000US-01980276
2000US-02098123
2000US-0209467
2000US-0219467
2000US-0215135
2000US-0215135
2000US-0215135
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2000US-0220964
2000US-0220964
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2000US-0225266.
2000US-0225267.
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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22-AUG-2000;
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PR 23-MG-2000; 2000UG-0221009
PR 01-SEP-2000; 2000UG-0222824;
PR 01-SEP-2000; 2000UG-0228244
PR 01-SEP-2000; 2000UG-022844;
PR 01-SEP-2000; 2000UG-022844;
PR 01-SEP-2000; 2000UG-022844;
PR 01-SEP-2000; 2000UG-022844;
PR 01-SEP-2000; 2000UG-022844;
PR 01-SEP-2000; 2000UG-022844;
PR 01-SEP-2000; 2000UG-022844;
PR 01-SEP-2000; 2000UG-022844;
PR 01-SEP-2000; 2000UG-022844;
PR 01-SEP-2000; 2000UG-022844;
PR 01-SEP-2000; 2000UG-022844;
PR 14-SEP-2000; 2000UG-023144;
PR 25-SEP-2000; 2000UG-02314;
PR 25-SEP-2000; 2
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used in preventing, treating or ameliorating a medical condition
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                  2000US - 0.24 9211.
2000US - 0.24 9212.
2000US - 0.24 9213.
2000US - 0.24 9215.
2000US - 0.24 9215.
2000US - 0.24 9216.
2000US - 0.24 9216.
2000US - 0.24 924.
2000US - 0.24 924.
2000US - 0.24 926.
2000US - 0.24 926.
2000US - 0.24 929.
2000US - 0.24 929.
2000US - 0.24 929.
2000US - 0.24 929.
2000US - 0.25 198.
2000US - 0.25 198.
2000US - 0.25 1868.
2000US - 0.25 1868.
2000US - 0.25 1869.
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N-PSDB; AAL01678.
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Matches 156; Conserv
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                  17-NOV-2000;
17-NOV-2000;
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FQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLYFGDE

fqkvrkeeiprqlqyiclylvhiagayllnlsrlglillllqysteflfhtxrlfyfade RYQKGLSLMPIVFISGRLVTLIVSVVTVGLHLAG-TNRNGNALSGNVNVLAAKIAVLSSS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                              314 caaqawlmwrfihsqlrxwreywneq--sakrrvpatprlparlikresgyhengvvkae 371
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                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 24333
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 CSIQVYITWTLTTVWLQRWLEDANLHVCGRKRR-
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11-JUL-2000; 2000US-0614150.
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Matches 136; Conservative
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N-PSDB; ABL10217.
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       Length 368;
                       Indels
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       ; Score 566; DB 22;
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64; Mismatches 130;
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                       Conservative
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N-PSDB; ABL11465.
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      Query Match
Best Local Simi
Matches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001
                                                                                                                                                                                                                                                                                                       ABB67362
                                                                                                                                                                                                                                                                                                                        ABB67362;
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                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSFPE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYFOKVR-KQDIPGQLIYIGLHLFHIGG-----AYLLYLNHLGLLLLMLHYAVELLSSV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 CSLL--YFGDERYQKGLSLWPIVFISGRLVTLIVSVVTVGLHLAGTNRNGNALSGNVNVL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                           61
useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                           RKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGV--VVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 AAKIAVLSSSCSIQVYITWTLTTVWLQRWLEDANLHVCGRKRRSRSRKGTENGVENPNRI
                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                       Length 1575;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                     Score 566; DB 22;
Pred. No. 2e-56;
64; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein, SEQ ID NO: 4270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG00189 standard; Protein; 125
                                                                                                                                                                                                                                                                                                                                       29.9%;
37.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                  Query Match 29.9%
Best Local Similarity 37.0%
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dumas Milne Edwards J,
                                                                                                                                   (ABB57737-ABB72072).
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(RESE ) RESEARCH CORP TECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                      The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. ESTs sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 A-EGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLN 119
                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                          1 MGLRKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVP 60
                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae; LAG1; life-span limiting domain; life-span extending domain; stress tolerance; longevity; recombinant protein production.
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note- "life-span extending domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "life-span limiting domain"
194..411
                                                                                                                                                                                                                                                                                                                       Ouery Match 21.9%; Score 414.5; DB 21; Best Local Similarity 64.0%; Pred. No. 2.8e-40; Matches 80; Conservative 24; Mismatches 20;
                                                                                    Claim 13; SEQ ID 4270; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae LAG1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR86810 standard; Protein; 411 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0336031
94US-0253875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae.
2000-500381/45
                                                                                                                                                                                                                                                                                      125 AA;
            N-PSDB; AAC00195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 EAGQL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 esgql 125
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                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR86810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
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Longevity-assurance protein homologue; LAPH-1; human; cell proliferation; longevity-assurance protein homologue; LAPH-2; signal transduction; cell cycle regulation; apoptosis; cellular homeostatic pathway; aging; cancer; inflammation; autoimmune disease; infection; neurodegenerative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 MLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQLSVFYI-VSGIWGMILL-ASEN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---FHSFPE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 llliwssyvfhftkm----qlaiyitmdvsdfflslsktlnylnsvftpfvfglfvf- 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 ----fwiylrhvvnirilwsvltefrhegnyvlnfatqqykcwisl-plvfv-----11 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 MVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPAEGLPSGSRTLYHYGVKDLATVFFY 85
                                                                                                                                                                                                                                                                                                                                    life-span limiting domain (see AAR86812) and a life-span extending domain (see AAR86812) and a life-span extending domain (see AAR86811). Overexpression of the LAG1 gene in older cells has a rejuvenating effect, which not only increases cellular life span, but also reproductive capacity and cellular tolerance to stress factors such as starvation and low pH. These cells may be used for the production of recombinant proteins. By increasing the life span of recombinant cells, the need for overexpression of recombinant gene products is avoided, and therefore any subsequent adverse effects on the host cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 L-----YFQKVRKQDIPGQLIYI-----------GLHLFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 IGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLYFGDERYQKGLSLWPIVFISGRLVTLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 411;
                                                                                                   Eukaryotic LAG1 gene and protein - controls longevity, stress tolerance and reproductive capacity of eukaryotic cells, for
                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae LAG1 gene product is composed of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.8%; Score 148.5; DB 17;
22.0%; Pred. No. 2.9e-08;
tive 46; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 CLSDPTLLWKSQPHNMMTFQMKFFYISQLAYW-------
                                                                                                                                                                       improved prodn. of recombinant proteins.
                                                                                                                                                                                                                                       Claim 23; Page 100-102; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY00876 standard; Protein; 394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68; Conservative
WPI; 1996-040238/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 aalqlvnly 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 AA;
                                   N-PSDB; AAT07263
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Homo sapiens.

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cellular homeostasis or with aging, cancers, disorders associated with inflammation or autoimmune disease including AIDS, Addison's disease, adult respiratory distress syndrome, allergies, anaemia, asthma, atterosciencis, bronchitis, cholecystitis, Crohn's disease, ulcerative colitis, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, errythema nodosum, atrophic gastritis, glomerulonephritis, gout, Grave's disease, hypereosinophilla, irritable bowel syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis, inflammation, osteoarthritis, osteoporosis, pancreatitis, rheumatoid arthritis, celeroderma, Syndrome, and autoimmune thyroiditis, infections, neurodegenerative disorders including Alzheimer's disease, ammesia, amyotrophic lateral sclerosis, bipolar disorder, catatonia, dementia, amyotrophic lateral sclerosis, bipolar disorder, catatonia, dementia, depression, Down's syndrome, tardive dyskinesia, dystonias, epilepsy, Huntington's disease, multiple sclerosis, neurofibromatosis, Parkinson's disease, schizophrenia, and Tourette's disorder, and myelodysplastic considered with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is the human longevity-assurance protein homologue of the invention, designated LAPH-1. LAPH-1 and LAPH-2 are involved in signal transduction and cell cycle regulation, and may play a role in regulating the balance between cell proliferation and apoptosis.

Increased expression of LAPH-1 or LAPH-2 may increase susceptibility to disregulation of cellular homeostatic pathways. Antagonists of LAPH-1 or LAPH-2 can be used to treat a disorder associated with disregulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 RLQLTKGKQNKLNEAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                       New isolated human longevity-assurance protein homologues - used to develop products for treating disorders associated with disregulation of cellular homeostasis or with ageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.3%; Score 138.5; DB 20; Length 394; 24.7%; Pred. No. 4.1e-07; vative 42; Mismatches 81; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81; Indels
                                                                                                                                                                                                                                                                Shah P;
                                                                                                                                                                                                                                                                Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 1; 101pp; English.
                                                                                                                                98WO-US15591.
                                                                                                                                                                           97US-0902853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 24.7'
Matches 44; Conservative
                                                                                                                                                                                                                     (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                              Corley NC, Hillman JL,
                                                                                                                                                                                                                                                                                                         WPI; 1999-153788/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 AA;
                                                                                                                                                                                                                                                                                                                              N-PSDB; AAX27073
                                         WO9906558-A1.
                                                                                                                                28-JUL-1998;
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167 FYISQLAYWFHSFPELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHY 226 227 AVELLSSVCSLLYFGDERYQKGLS----LWPIVFISGRLVTLIVSVVTVGLHLAGTNR 280 ò g ò

Search completed: September 6, 2002, 17:09:47 Job time: 8276 sec

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Sequence 2, Appliance 2, Appliance 2, Appliance 6, Appliance 6, Appliance 11, Appliance 2, Appliance 
                                                           6, Appli
2, Appli
5240846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: JAZWAINSKI, S. M.

APPLICANT: JAZWAINSKI, S. M.

TITLE OF INVENTION: LAGI: A GENE FOR INCREASING THI

TITLE OF INVENTION: LONGEVITY OF EUKARYOTES

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

CONTRY: United States

LIS30

COMPUTER: FADABLE FORM:

MEDIUM TYPE: FLORPY disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

RELING DATE:

FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FI
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                                                                                                                                    US-08-336-031-6

VC-US95-06725-6

US-08-746-111-5

US-07-879-617A-11

US-08-301-722A-3

US-08-301-722A-3

US-08-53-98-11

US-08-09-084-813-3
                                                                                                                                                                                                                                                                                                                                                                  PCT-US92-09662-3
US-08-986-768-2
US-08-295-814E-2
US-09-343-361-2
                                                                                  PCT-US93-11667-2
5240846-5
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/253,875
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9303Z
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4366
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TWOMMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 22.09
Matches 68; Conservative
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1 MGLRKKNARNPPVLSHEFMV.....NGVENPNRIDSPPKKKEKAP 363
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Sequence 6,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-902-853-1
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US-08-902-853-3
US-08-902-853-3
US-08-902-853-3
US-08-901-918-5
US-08-951-912-4
US-09-256-703-2
US-08-951-912-6
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Match Length
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Perfect score:
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86 MLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQLSVFYI-VSGIWGMILL-ASEN 143
                                                                                        140 MIFFTFLREFLMDVVIRPFTVYLNVTSEHROKRMLEOMYALFYCGVSGPFGLYIMYHSDL 199
                                                                                                                                                          200 WLFKTKPMYRTYPVITNPFLFKIFYLGQAAFWAQQACVLVLQLEKPRKDYKELVFHHIVT 259
                                                                                                                                                                                                               182 L-----YFQKVRKQDIPGQLIYI------GLHLFH 205
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                                                                                                                                                                                                                                                                                                                 313 ----EWIYLRHVVNIRILMSVLTEFRHEGNYVLNFATQQYKCWISL-PIVFV-----LI 361
                                                                                                                                      ------FHSFPE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HIllman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
APPLICANT: Lal, Preeti
TITLE OF INVENTION: HUMAN LONGEVITY-ASSURANCE PROTEIN HOMOLOGS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                144 CLSDPTLLWKSQPHNMMTFQMKFFYISQLAYW-
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FILING DATE: Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMULICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: ?
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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MEDIUM TYPE: Diskett
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; CLONE: 541568
US-08-902-853-7
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US-08-902-853-7
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                                                                                                                                                                                                   200 WLFKTKPMYRTYPVITNPFLFKIFYLGQAAFWAQQACVLVLQLEKPRKDYKELVFHHIVT 259
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                                                                                                                                                                                                                                                                 144 CLSDPTLLWKSQPHNMMTFQMKFFYISQLAYW-----------FHSFPE 181
                                             Gaps
                                                                                     26 MVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPAEGLPSGSRTLYHYGVKDLATVFFY 85
  Length 411;
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAG1: A GENE FOR INCREASING THE LONGEVITY OF EUKARYOTES
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06725
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
7.8%; Score 148.5; DB 2;
22.0%; Pred. No. 1.1e-08;
iive 46; Mismatches 106;
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APPLICATION NUMBER: US 08/253,875 & 08/336,031
FILING DATE: 03-JUN-1994 & 08-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: LAG1: A GENE FOR INCREASE TITLE OF INVENTION: LONGEVITY OF EUKARYOTES NUMBER OF SEQUENCES:
CORRESPONDENCE STOLLY, Scott, Murphy & Presser STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                      182 L-----YFQKVRKQDIPGQLIYI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,346
REPERENCE/DOCKET NUMBER: 9303Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
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amino acid
                                           Conservative
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ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
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STATE: New York
                    Best Local Similarity
Matches 68; Conserv
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US-08-902-853-6
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TOPOLOGY: line IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-08-902-853-6
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CLONE:
US-08-902-853-1
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                                                   11;
                                                                                                           86 MLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQLSVFYI-VSGIWGMIIL-ASEN 143
                                                                                                                                                                             200 WLFKTKPMYRTYPVITNPFLFKIFYLGQAAFWAQQACVLVLQLEKPRKDYKELVFHHIVT 259
                                                                                                                                                                                                                                                                                                                                                                                          313 ----EWIYLRHVVNIRILMSVLTEFRHEGNYVLNFATQQYKCWISL-PIVFV-----LI 361
                                                                                                                                                                                                                               -------FHSFPE 181
                                                                                                                                                                                                                                                                                                                                   260 LLLIWSSYVFHFTKM-----GLAIYITMDVSDFFLSLSKTLNYLNSVFTPFVFGLFVF- 312
                                                     Gaps
                                                                                   26 MVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPAEGLPSGSRTLYHYGVKDLATVFFY 85
                                                                                                                                                                                                                                                                                                                                                                      206 IGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLYFGDERYQKGLSLWPIVFISGRLVTLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08902853
Patent No. 5945330
GENERAL INFORMATION:
APPLICANT: HIllman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
APPLICANT: Lah, Preeti
TITLE OF INVENTION: HUMAN LONGEVITY-ASSURANCE PROTEIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                  Length 411;
                                                   Indels
              ch 7.8%; Score 148.5; DB 5;
1 Similarity 22.0%; Pred. No. 1.1e-08;
68; Conservative 46; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,853
FILING DATE: Herewith
CLASSIFICATION: ?
                                                                                                                                                                                                                           144 CLSDPTLLWKSQPHNMMTFQMKFFYISQLAYW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                  L-----YFQKVRKQDIPGQLIYI-----
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/COCKET NUMBER: PF-07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
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CITY: Palo Alto
STATE: CA
                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            266 VSVVTVGLH 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 AALQLVNLY 370
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US-08-902-853-1
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                  Query Match
                                   Best Loca
Matches
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167 FYISQLAYWFHSFPELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHY 226
                                                                                                                                                                                                          107 RLQLTKGKQNKLNEAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKF 166
                                                                                                                                                                 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    227 AVELLSSVCSLLYFGDERYQKGLS----LWPIVFISGRLVTLIVSVVTVGLHLAGTNR 280
                                                                                                                                                                                                                                                                                                                                                                                                                                 241 SSDYLLEACKMVNY -- MQYQQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESISNR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN LONGEVITY-ASSURANCE PROTEIN HOMOLOGS
                                                                                                                Length 394;
                                                                                                                                                                 Indels
                                                                                                             Query Match 7.3%; Score 138.5; DB 2; Best Local Similarity 24.7%; Pred. No. 1.5e-07; Matches 44; Conservative 42; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,853
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08902853

Sequence 6, Application US/08902853

Patent No. 5945330

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Corley, Neil C.

APPLICANT: Carley, Neil C.

APPLICANT: Lail, Preeti

ITLE OF INVENTION: HUMAN LONGEVITY-ASSURAN NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0345 US
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
LIBRARY: LIVRTUT04
CLONE: 2516821
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52;

Indels

Length 380;

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5.8%; Score 110; DB 2;
23.6%; Pred. No. 0.0003;
tive 39; Mismatches 71;
                                                                               93 HATIQEYVL------DKLSRRLQLTKGKQ-
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 62; Conserva
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  Query Match
Best Local Similarity
Matches 50; Conserv
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                                                                                 11;
                                                                                                                                                                                                                            157 EQGYSFFYYLCFWFLGLYIYRSSNYWSNEEKLFEDYPQYYMSPLFKAYYLIQLGFWLQQI 216
                                                                                                                                                           104 PDGS---YGKGPKDACFPIFWVIVFTAFRVIVMDYVF----RPFVLNWGVRNRKVIIRFC 156
                                                                                                                                                                                                  120 EAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSF 179
                                                                                                                    65 PSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQN-----KLN 119
                                                                                                                                                                                                                                                                               180 PELYFQKVRKQD------IPGQLIYI--GLHLFHIGGAYLLYLNHLGLLLL----ML 224
                                                                                                                                                                                                                                                                                                      217 LVLHLEQ-RRADHWQMFAHHIVTCALIILSYGFNFLRVGNA-ILYIFDLSDYILSGGKML 274
                                                                                                                                                                                                                                                                                                                                                           225 HYAVELLSSVCSLLYFGDERYQKGLSLWPIVFISGRLVTLIVSVVTV-----GLHL 275
                                                                                                                                                                                                                                                                                                                                                                                    275 KYLG--FGKICDYLF-----GIFVASWVYSRHYLFSKILRVVVTNAPEIIGGFHL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN LONGEVITY-ASSURANCE PROTEIN HOMOLOGS NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS:
                                                                                 46;
                                      Length 387;
                                    ; Score 125; DB 2; Length 38; Pred. No. 5.4e-06; 35; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,853
FILING DATE: Herewith
CLASSIFICATION: ?
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0345 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08902853
Patent No. 5945330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: COTIEY, Neil C.
APPLICANT: Shah, Purvi
APPLICANT: Lal, Preeti
                                      6.68;
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SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
                                      Query Match 6.6%
Best Local Similarity 23.9%
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166
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US-08-902-853-3
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IMMEDIATE SOURCE:
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TOPOLOGY: lin
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STATE: CA
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US-08-902-853-3
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                                                                         125 SVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLA-YWFHSFPELY 183
                                                                                                                           140 FTFYLIAFIAGMAVIVDKPWFYDMKKVWEGYPIQSTIPSQYWYYMIELSFYW----SLL 194
                                                                                                                                                                                   184 F---QKVRKQDIPGQLIYIGLHLFHIGGAYLL----YLNHL--GLLLIMLHYAVE-LLSS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: J.D. Young & C.E. Cass
TITLE OF INVENTION: CDNA ENCODING NUCLEOSIDE TRANSPORTER
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 649;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/800,291B
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                          249 AKMFNYAGWKNTCNNIFIVFAIVFIITRLVIL 280
                                                                                                                                                                                                                                                                                              234 VCSLLYFGDERYQKGLSL-WPIVFISGRLVTL 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 13-FEB-1997
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/499,314
FILING DATE: 7-UILY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08800291B Patent No. 6153740 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  649 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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382 SKLVYPEVEESKERREE------GVKLTYGDAQNLIEAASTGAAISVKVVANIAANLI 433
                                            175 WFHSFPELYFOKVRKODIPGOLIYIGLHLFHIGGAYLLYLNHLGLLL---LMLHYAVELL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 VFFYMLVAIIIHATIQEYVLDKLSRRLQLTKG--KQNKLNEAGQLSVFYIVSGIWGMIIL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKLVYPEVEESKFRREE------GVKLTYGDAQNLIEAASTGAAISVKVVANIAANLI 434
    325 LIRPYLADMTL---SEVHVVMTGGYATIAGSLLGAYISFGIDATSLIAASVMAAPCALAL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|: |||||: | | | | : : :||||: 271 IGLOFVLGLLVIRTEPGVLPII 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70; Gaps
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                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08800291B
Patent No. 6153740
GENERAL INFORMATION:
APPLICANT: J.D. Young & C.E. Cass
TITLE OF INVENTION: CDNA ENCODING NUCLEOSIDE TRANSPORTER
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 650;
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                                                                                                                                                                :: : : | : | : | | . | | | 434 AFLAVLDFINAALSWLGDMVDIQGLSFQLICSYILRPVAFLMG 476
                                                                                                                                      232 SSV-----CSLLYFGDERYQKGLS-----LWPIVFISG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/800,291B
FILING DATE: 13-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: 05A
COUNTRY: USA
ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/499,314
FILING DATE: 7-JULY-1995
ATTONREY/ABOTH INFORMATION:
NAME: Haile, Lisa A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07254/044W01
TELEPHONE: 619/678-5099
TELEFAX: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.2;
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21.9%; Pred. No.
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 21.9%
Matches 62; Conservative
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; MOLECULE TYPE:
US-08-800-2918-4
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271 VFFSCVISVLXHVGLMQWVILKIAWLMQVTMGTTATETLSVAGNIFVSQTEAP-----L 324
                                                                                            |:| || || |: | :|| || 325 LIRPYLADMTL---SEVHVVWTGGYATIAGSLLGAYISFGIDATSLIAASVWAAPCALAL 381
                                                                                                                                                       175 WFHSFPELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLL---LMLHYAVELL 231
                                                                                                                                                                                      382 SKLYYPEVEESKFRREE------GVKLTYGDAQSLIEAASTGAAISVKVVANIAANLI 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 IGLOFVIGILVIRTEPGFIAFEWIGEQIRIFLSYTKAGSSFVFGEALVKDVFAFQVLPII 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 VFFYMLVAIIIHATIQEYVLDKLSRRLQLTKG--KQNKLNEAGQLSVFYIVSGIWGMIIL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 VFFSCVISVLYHVGLMQWVILKIAWLMQVTMGTTATETLSVAGNIFVSQTEAP-----L 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: J.D. Young & C.E. Cass
APPLICANT: J.D. Young & C.E. Cass
TITLE OF INVENTION:
TOWNERS OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 649;
                                                                                                                                                                                                                                                                           232 SSV-----CSLLYFGDERYQKGLS-----LWPIVFISG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,291B
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 0.2; 49; Mismatches 102;
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REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07254/044W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 89;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/499,314
FILING DATE: 7-JULY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08800291B Patent No. 6153740
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SEQUENCE CHARACTERISTICS:
LENGTH: 649 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.7%;
Best Local Similarity 21.9%;
Matches 62; Conservative 4
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US-08-800-291B-6
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Similarity 20.8
33; Conservative
                CORRESPONDENCE ADDRESS:
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; MOLECULE TYPE: protein
US-08-951-912-4
                                                                  COUNTRY: US.
                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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Best Local Simi
Matches 83;
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US-09-174-077-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1138 NIMSTLOWAVNSSIDVDSLMRSVSRVFKFIDMPTEGKPTKSTKPYRNGQLSKVMIIENSH 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 ADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPAEGLPSGSRTLYHYGV----KD 78
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Local Similarity ^ 20.8%; Pred. No. 1.2;
hes 83; Conservative 63; Mismatches 112; Indels 142;
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                                                                                                                                                   APPLICANT: DOOR, Jian-yun
APPLICANT: Kan, Yuet Wal
APPLICANT: Kan, Yuet Wal
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Efficient AaV Vectors
FILE REFERENCE: 023070-084910US
CURRENT FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: US 60/075,980
PRIOR PLING DATE: 1988-02-25
SOFTWARE: PACENTING DATE: 1988-02-25
SOFTWARE: PACENTIN VOI: 2.1
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
OTHER INFORMATION: truncated cystic fibrosis transmembrane
US-09-256-703-2
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                        435 AFLAVLDFINAALSWLGDMVDIQGLSFQLICSYILRPVAFLMG 477
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232 SSV-----CSLLYFGDERYQKGLS----
                                                                                                        Sequence 2, Application US/09256703; Patent No. 6294379; GENERAL INFORMATION: APPLICANT: Dong, Jian-yun
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Patent No. 5972995
GENERAL INFORMATION:
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APPLICANT: 111ek, Beate
TILLE OF INVENTION: COMPOSI:
TITLE OF INVENTION: FIBROSI:
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                          LENGTH: 1476
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Best Local S
Matches 83
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1085 TANWE----LYLSTLRWEQMRIEMIEV---IFFIAVTFISILTTGEGEGRVGIILTLAM 1136
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Patent No. 6329422
GENERAL INFORMATION:
APPLICANT: Fischer, Horst
APPLICANT: Illek, Beate
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CYSTIC FIBROSIS THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 LA------TVF-FYMLVAIIIH-----ATLQEYVLDK------LSRRLQLTKGKQ 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.6%; Score 87; DB 2; Length 1479;
20.8%; Pred. No. 1.3;
tive 63; Mismatches 112; Indels 142;
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITT: Seattle
                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,912
FILING DATE: 16-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 ----SLWPIVFISGRLVTL--IVSVVTVGLHLAGTNRNGNAL----
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                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                              FILING DATE: 16-0CT-1997
CLASSIFICATION: 514
ATORNEZ/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2001]
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 4:
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
mutter: IBM PC compatible
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LENGTH: 1479 amino acids
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Gaps

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1198 VKKDDIWP----SGGQMTVKDLTAKYTEG------GNAILENISFSISPGQRVGLLG 1244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 -AYWFHSFPELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYL-----NHLGLLLLM-- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 ADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPAEGLPSGSRTLYHYGV-----KD 78
                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 4.6%; Score 87; DB 1; Length 1480; Best Local Similarity 20.8%; Pred. No. 1.3; Matches 83; Conservative 63; Mismatches 112; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gregory, R.J., Armentano, D., Couture, L.A., Smith, APPLICANT: A.E.
TITLE OF INVENTION: GENE THERAPY FOR CYSTIC FIBROSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: BRUMBAUGH, GRAVES, DONOHUE & RAYMOND 30 ROCKEFELLER PLAZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1245 RTGSGKSTLLSAFLRLINTEGEIQIDGVSW--DSITLQQW 1282
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                                                1107.030010
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,742A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08136742A Patent No. 5670488 GENERAL INFORMATION:
                        REGISTRATION NUMBER: 32,141
REFERENCE/POCKET UNMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                     : 1480 amino acids
AMINO ACID
                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                    HOMO SAPIENS
        kagan, sarah a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: NEW YORK STATE: NEW YORK
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                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                        US-07-637-621-2
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                                                                                                                                                                                                                                                                                                   4.6%; Score 87; DB 4; Length 1479; ilarity 20.8%; Pred. No. 1.3; Conservative 63; Mismatches 112; Indels 1
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APPLICANT: cutting, gary
APPLICANT: antonarakis, stylianos e
APPLICANT: akazazian jr., haig h
TITLE OF INVENTION: CYSTIC FIBROSIS MUTATION CLUSTER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie and Beckett
STREET: 1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1244 RTGSGKSTLLSAFLRLLNTEGEIQIDGVSW--DSITLQOW 1281
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19910104
CLASSIFICATION: 435
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CITY: Washington, D.C.
FILE REFERENCE: 200116.403C1
CURRENT APPLICATION NUMBER: US/09/174,077
CURRENT FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: US 08/951,912
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.0
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Patent No. 5407796
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                                                                                                                                                                                   TYPE: PRT
COCANISM: Homo sapiens
US-09-174-077-4
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 83; Conserv
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-07-637-621-2
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20.8%; Pred. No. 1.3;
tive 63; Mismatches 112; Indels 142; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 ADMYSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPAEGLPSGSRTLYHYGV----KD 78
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CLASSIFICATION: 514
PRIOR APPLICATION 514
APPLICATION NUMBER: US 07/985,478
FILING DATE: 02-DEC-1992
CLASSIFICATION 10 514
ATTOREX/AGENT INFORMATION:
NAME: Seide, Rochelle K,
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: 32,300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 765-2519
INFORMATION FOR SEO ID NO: 2:
FEMALESAX: (212) 765-2519
SEQUENCE CHARACTERISTICS:
FEMALE: 1400 millionical control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t
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Patent NO. 5688677
GENERAL INFORMATION:
APPLICANT: CHENG, SENG H.
APPLICANT: EBERT, KARL M.
APPLICANT: MEADE, HARRY M.
APPLICANT: MEADE, HARRY M.
TITLE OF INVENTION: DECXYRIBONUCLEIC ACIDS CONTAINING
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ANDRESPONDENCE ADDRESS:
ANDRESSED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 20.89
hes 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-136-742A-2
                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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STREET: ONE MOUNT
CITY: FRAMINGHAM
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US-08-135-809A-2
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Matches
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923 ADTLLAMGFFRGLPLVHTLITVSKILHHKMLHSVL---QAPMSTLNTLKAGGILNRFSKD 979
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4.6%; Score 87; DB 1; Length 1480;
Best Local Similarity 20.8%; Pred. No. 1.3;
Matches 83; Conservative 63; Mismatches 112; Indels 142;
                           MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/135,809A
FILING DATE: 13-OCT-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 ----SLWPIVFISGRLVTL--IVSVVTVGLHLAGTNRNGNAL----
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Job time: 7972 sec
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                                                                                                                                                                    ATTORNEZ/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31 845
REFERENCE/DOCKET NUMBER: 164
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                          IELEPHONE: (508) 872-8400
IELEPRA: (508) 872-8400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1480 amino acids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                        // MOLECULE TYPE: protein US-08-135-809A-2
                                                                                                                                                                                                                                                                                                                                                                     amino acid
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September 6, 2002, 15:18:41; Search time 52.02 Seconds (without alignments) 670.520 Million cell updates/sec
                                                                                                                                                                                              US-09-807-470-2
1892
1 MGLRKKNARNPPVLSHEFMV.....NGVENPNRIDSPPKKKEKAP 363
                                                                                                                                                                                                                                                                                                                                                                               283138
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   283138 seqs, 96089334 residues
                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                    Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	translocating chai translocating chai hypothetical prote hypothetical prote LAG1 proteful - yea longewity assuranc longewity assuranc hypothetical prote Na/H antiporter (n Na/H antiporter (n Na/H antiporter (n Na/H antiporter (n Na/H antiporter (n Na/H antiporter (n Na/H antiporter (n ABC transporter (n ABC transporter (n hypothetical prote probable tyrosine marerobic dimethyl hypothetical prote probable membrane cytochrome-c oxida probable membrane cytochrome-c oxida probable membrane hypothetical prote hypothetical prote probable membrane hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote	
S	S21736 S31034 T19417 T19417 S46800 S30134 T380138 T380138 T480389 T480389 T47029 B83987 T10098 AG0403 G83685 AH0050 G83685 AH0050 G83685 AH0050 G83685 AH1059 AH1059	
DB		
Length	2000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
% Query Match	00000000000000000000000000000000000000	
Score	11150 11150 1444 1444 1444 154 164 164 165 165 165 165 165 165 165 165	
Result No.		

probable ubiquinol	hypothetical prote	hypothetical prote	cystic fibrosis tr	hypothetical prote	cytochrome-c oxida	probable membrane	NADH dehydrogenase	amino acid transpo	major facilitator	multidrug resistan	hypothetical prote	hydrogenase-1 oper	hypothetical prote	conserved hypothet	hypothetical prote	
S48191	T09340	Н96615	JC6139	D85437	A32431	AB0682	E81251	B90504	T40575	E69821	E90604	AF0676	T21869	AC1252	D90012	
7	7	7	۲	~	N	~	~	~	~	П	N	7	~	~	7	
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5.0	5.0	5.0	5.0	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	
94.5	94	94	94	93.5	93.5	93	93	66	93	93	93	92.5	92.5	92	92	
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

RESUI S217: C.Spe C.Spe C.Dat C.Acc C.Acc R.Acf A.Tit A.Tit A.Ste A.Ste A.Ste A.Ste A.Ste A.Ste A.Ste A.Ste C.Spe C.Acc C.C.C C.Acc C.C.C C.C.C.C C.C.C.C C	RESULT 1  S21736  translocating chain-associating membrane protein - dog  C; Species: canis lupus familiaris (dog) C; Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 24-Sep-1999 C; Accession: S21736 C; Accession: S21736 C; Accession: S21736 A; Title: A protein of the endoplasmic reticulum involved early in polypeptide A; Reference number: S21736; MUD: 92244357 A; Reference number: S21736 A; Status: preliminary A; Accession: S2173 A; Accession: S2173 A; Coss-references: EMBL: X63678; NID: 9941; PIDN: CAA45217.1; PID: 9942 C; Superfamily: translocating chain-associating membrane protein C; Keywords: transmembrane protein	nge 24-Sep-1999 ly in polypeptide translo PID:9942 ein:
Que Bes Mat	Query Match 60.8%; Score 1150.5; DB 2; Length Best Local Similarity 59.8%; Pred. No. 1.8e-92; Matches 223; Conservative 58; Mismatches 81; Indels	Length 374; Indels 11; Gaps 4;
Qy Db	OY 1 MGLRKKNARNPPVLSHEFMVQNHADMYSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVP 60   1   1   1   1   1   1   1   1   1	LTLQHGVVVP 60 :   :   :  VTLQXNVTLP 60
Qy Dp	QY 61 A-EGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLN 119     :   :   :   :	LTKGKQNKLN 119 
Qy Dp	QY 120 EAGQLSVFYIVSGIWGMILLASENCLSDPTLLMKSQPHNMMFFQMKFFYISQLAYWFHSF	SQLAYWFHSF 179 :       :  AQLAYWFHAF 180
Oy Op	OY 180 PELYFOKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLY	LLSSVCSLLY 239 
Qy	QY 240 FGDERYQKGLSLMPIVFISGRLVTLIVSVVTVGLHLA-GTNRNGNALSGNVNVLAAKIAV	VNVLAAKIAV 298       :    FNVLAVRIAV 300
Oy Dp	OY 299 LSSSCSIQVYITWTLTTVWLQRWLEDANLHVGGRKRRSRSRKGTENGVENP	ENGVENP 349        ENGVNGTVTS 360
oy Db	QY 350 NRIDSPPKKKEKA 362       :   :  Db 361 NGADSPRNRKEKS 373	_

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301

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PIDN:CAA18772.1; GSPDB:GN00022; CESP:C24F3.1b
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T19419
                                                                                                                                                                                                                                                        62 EGLPSGSRTLYHY--GVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLN 119
                                                                                                                                                                                                                                                                                          EAGQLSVFYIVSGIWGMIILASENC--LSDPTLLWKSQP--HNMMTFQMKFFYISQLAYW 175
                                                                                                                                                                                                                                                                                                                                                                                                                176 FHSFPELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 SLLYFGDERYQKGLS----LMPIVFISGRLVTLIVSVVT--VGLHLAGTNRNGNALSGN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 VNVLAAKIAVLSSSCSIQVYITWTLTTVWLQRWLEDANLHVCGRKRRSRSRKGTENGVEN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 FNTAVIRLNVLLQLFLLYSFVV-----FHM-GRFRESNAKKEKKKSAAA 349
                                                                                                                                  2 GLRKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 AVEQGQEREVHGYLSGILDLPAIFFYSVCWIVVHAVVQEYGLDKISKKTHLSKVSTFKFG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGLPSGSRTLYHY -- GVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLN 119
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                                                                                                                                                                       EAGQLSVFYIVSGIWGMIILASENCLSD-----PTLLWKSQP--HNMMTFQMKFFYISQL
                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-JJ C; Accession: T19419
R; McMurray, A.
Submitted to the EMBL Data Library, April 1998
A; Reference number: 219122
A; Recession: T19419
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Map position: 4
A; Introns: 114,73; 158/2; 365/3
C; Superfamily: translocating chain-associating membrane protein
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                               Length 371;
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                                                                                      Indels
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                        Score 441.5; DB
Pred. No. 9.8e-31
23.3%; Sco. 30.0%; Pred. No. 5... 30.0%; Pred. Nismatches 76; Mismatches 76; Mism
                                                                             Conservative
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                                                 Similarity
                                                                          Matches 112;
                  Query Match
Best Local
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                                                                                                                               C; Accession: $30034
R; Goerlich, D.; Hartmann, E.; Prehn, S.; Rapoport, T.A.
Nature 37, 47-52, 1992
A; Pitle: A protein of the endoplasmic reticulum involved early in polypeptide translocat
A; Reference number: $21736; MUID:92244357
A; Accession: $30034
A; Accession: $30034
A; Accession: $7004
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-374 <GOE>
A; Cross-references: EMBL: X63679; NID:937264; PIDN: CAA45218.1; PID:937265
C; Superfamily: translocating chain-associating membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. Accession: T19417

R. McMurray, A.

Submitted to the EMBL Data Library, April 1998
A. Accession: T19417
A. Accession: T19417
A. Accession: T19417
A. Molecule type: DNA
A. Residues: 1-371 < WIL>
A. Residues: 1-371 < WIL>
A. Cross-references: EMBL: AL022716; PIDN: CAA18770.1; GSPDB: GN00022; CESP: C24F3.1a
A. Experimental source: clone C24F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4,
                                                 translocating chain-associating membrane protein - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 A-EGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAGQLSVEYIVSGINGMIILASENCLSDPTLLWKSOPHNMMTFQMKFFYISQLAYWFHSF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 LSSSCSIQVYITWTLTTVWLQRWLEDANLHVCGRKRR-----SRSRKGTENGVE---NP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PELYFQKVRKQDIPGQLIY1GLHLFH1GGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLY
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Best Local Similarity 58.7%; Pred. No. 4.6e-91;
Matches 219; Conservative 61; Mismatches 82; Indels
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A;Introns: 114/3; 158/2; 363/3
C;Superfamily: translocating chain-associating membrane protein
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A.Reference number: S37813
A,Accession: S37813
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Esidues: 1-418
A,Esidues: 1-418
A,Esidues: 1-418
A,Esidues: 1-418
A,Experimental source: strain S288C
B,Amatruda, J.F.; Gattermeler, D.G.; Cooper, J.A.
Submitted to the EMBL Data Library, August 1991
A,Peference number: S17016
A,Reference number: S17016
A,Reference number: S17016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Accession: 530134
A, MoLecule type: DNA
A, Rosidues: 1-418 <-BOX>
A, Cross-references: GB:S59773; NID:g300231; PIDN:AAC60549.1; PID:g300232
A, Experimental Source: strain S288C
R; Boyer, J.; Pascolo, S.; Richard, G.F.; Ghazvini, M.; Colleaux, L.; Thierry, A.; Mcn submitted to the Protein Sequence Database, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              longevity assurance protein homolog SPBC3E7.15c – fission yeast (Schizosaccharomyces C; Species: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                         reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                 C; Species: Saccharomyces cerevisiae
C;Date: 18-Uun-1993 #sequence_revision
C;Accession: S30134; S37819; S17017
K;Boyer, J.; Pascolo, S.; Richard, G.F.; Dujon, B.
Yeast 9, 279-287, 1993
A;Title: Sequence of a 7.8 kb segment on the left arm of yeast chromosome XI mammalian UGC-1 gene.
A;Reference number: S30132; MUID:93255906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 GSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQLSV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 QLEKPRKDHNELTFHHIVTLLLIWSSYVFHFTKMGLP---IYITMDVSDFLLSFSKTLNY 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A;Residues: 1-149 <AMA>
A;Cross-references: EMBL:X61398; NID:g455515; PIDN:CAA43670.1; PID:g3445
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                                                                                                                                                                                                                   /east (Saccharomyces cerevisiae)
protein YKL156
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C;Superfamily: hypothetical protein YKL008c
C;Keywords: transmembrane protein
                                                                                                                                                                                                                         Alternate names: hypothetical prote
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                                                          362 AALQLVNLY 370
      VSVVTVGLH
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Matches 63
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submitted to the EMBL Data Library, June 1994
A:Description: The sequence of S. cerevisiae cosmid 9780.
A:Reference number: $46797
A:Accession: $46800
A:Molecule type: DNA
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A; Residues: 1-172,'IV',175-219,'C',221-300,'TEISGI',314,'EKQE',315,'DSNDNPTE',324,'A',32
A; A: A: A: A: AGGY'386,'L',388,'NRLARNNEK' <DAM>
A; Cross-references: GB:U08133
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N;Alternate names: hypothetical protein YHL003c
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 *sequence_revision 28-Oct-1994 *text_change 23-Mar-2001
C;Accession: S46800; A54012
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                                                                                                                                                                                                                                   301 AGNFNTAVIRLNVLLAVVLLQLFLLYSFVV------FHM-GRFRESNAKKEKKKS 348
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      244
                                                             233 SVCSLLYFGDERYQKGLS-----LWPIVFISGRLVTLIVSVVT--VGLHLAGTNRNGNAL 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLIWSSYVFHFTKM-----GLAIYITMDVSDFFLSLSKTLNYLNSVFTPFVFGLFVF- 312
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                                                                                              185 SYWIHQFPEFYLQKLKRDEIRQKSVQAILHIAFISIAYFFNFTRVGLALITLEYITQLIF
                                                                                                                                                                                      SGNVNVLAAKIAVLSSSCSIQVYITWTLTTVWLQRWLEDANLHVCGRKRRSRSRKGTENG
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; Pred. No. 3.6e-05;
46; Mismatches 106;
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A;Cross-references: SGD:S0000995; MIPS:YHL003c
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Best Local Similarity 22.0%
Matches 68; Conservative
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349 AAAAAAV---PKKEKK 361
                                                                                                                                                                                                                                                                                                              346 VENPNRIDSPPKKKEK 361
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C; Function:
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Best Local Similarity
Matches 80; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 EAWQE 352
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                                                                                                                 A;Accession: T40389
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: 1-357 cLTN>
A;Residues: 1-357 cLTN>
A;Residues: T-357 cLTN>
A;Residues: EMBL:AL023534; PIDN:CAA19018.1; GSPDB:GN00067; SPDB:SPBC3E7.15c
A;Experimental source: strain 972h-; cosmid c3E7
B;GWilliam, R.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AL031534; PIDN:CAA20722.1; GSPDB:GN00067; SPDB:SPEC4F6.02c
A;Experimental source: strain 972h-; cosmid c4F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, September 1997

A.Reference number: 221761

A.Accession: T38012

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: DNA

A.Residues: 1-390 < CHU>
A.Cross-references: EMBL: 299258; PIDN:CAB16359.1; GSPDB:GN00066; SPDB:SPACIA6.09c

A.Experimental source: strain 972h-; cosmid clA6

C.Genetics:
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000 C;Accession: T40389; T40499 R;Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Brown, D.; Churcher, C.M. submitted to the EMBL Data Library, May 1998 A;Reference number: 221924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 VAIIIHATIQEYVLDKLSRRLQL-TKGKQNKLNEAGQLSVFYIVSGIWGMIIL-ASENCL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 PSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQN-----KLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 EKTWIVPLILITLLVGWYFVNPNGYIKYGIFL-SYPIPGTNPAQYGKGRLDIAFCLFYAL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----QHGVVVPAEGLPSGSRTLYHYGVKDLATVFFYML 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 SDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSFPELYFQ--KVRKQDIPGQLIYIGLHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 LLIGLSYYFHFTWIGLAVFITMDTSDIWLALSKCL----NYVNTVIVYPIFVI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 FHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLYFGDERYQKGLSLWPIVFI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.0%; Score 133; DB 2; L 20.5%; Pred. No. 0.00068; Live 45; Mismatches 117;
                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, September 1998 A; Reference number: 221933 A; Accession: T40499 A; Accession: T40499 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-357 <GWI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: SPBC3E7.15c; SPBC4F6.02c
A;Map position: 2
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Best Local Similarity 23.9%,
Matches 57; Conservative
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Best Local Similarity 20.5%
Matches 48; Conservative
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A; Map position: 1
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hypothetical protein yicA [imported] - Lactococcus lactis subsp. lactis (strain IL14) C; Species: Lactococcus lactis subsp. lactis C; Species: Lactococcus lactis subsp. lactis C; Species: Lactococcus lactis subsp. lactis C; Species: Lactococcus lactis subsp. lactis C; Species: Lactococcus lactis subsp. lactis C; Accession: B86726 R; Balotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; En Genome Res. 11, 731-753, 2001 A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A; Reference number: A86625; MUID:21235186; PMID:11337471 A; Accession: B86726 A; Species Loya A; Residues; L696 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE005176; PID:g12723732; PIDN:AAK04908.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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Na+/H+ antiporter homolog yjbQ - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Dacillus subtilis
C;Date: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 15-Oct-1999
C;Accession: A69845
-----VVTVGLHLAGTNRNGNALSGNVNVLAAKI--AVLSSSCSIOVYITWTLTTVWL 318
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                                                                                                                                                                    217 LVLHLEQ-RRADHWQMFAHHIVTCALIILSYGFNFLRVGNA-ILYIFDLSDYILSGGKML 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 MLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQLSVFYIVSGIWGMIILASENCL 145
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                                                                                                                                                                                                                                                            225 HYAVELLSSVCSLLYFGDERYQKGLSLWPIVFISGRLVTLIVSVVTV-----GLHL 275
                                                                                                                                                                                                                                                                                                        275 KYLG--FGKICDYLF-----GIFVASWVYSRHYLFSKILRVVVTNAPEIIGGFHL 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 ML---IWNARMTSIIFEIFA--MQIPKGLFNIIN-----SLIYVLIGLLINVLVSGKKAF
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21.9%; Pred. No. 0.041;
Ive 62; Mismatches 122;
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Query Match 5.55
Best Local Similarity 22.45
Matches 82; Conservative
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A;Molecule type: DNA
A;Residues: 1-522 <STO>
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             A; Gene: CAC0444
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Matches 6
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.W.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.W.; Changer, S. D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rocke, M.; Sadale, Y.; Sacho, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Tergestra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasha, K.; Yoshida, K.; Asthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Atchors: A69845

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Rective DNA
A;Recidues: Josephan
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J. Bacteriol. 183, 4823, 4839, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB13021.1; PID:e1183184.
A;Experimental source: strain 168
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Na/H antiporter (napA) [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C;Accession: E96954
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; N.;Nolling, J.; Bretonett, G.N.; Koonin, E.V.; Smith, D.R.
J; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J; Bacteriol. 183, 4823-4838, 2001
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A;Residues: 1.393 <KUR>
A;Residues: 1.393 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK78424.1; PID:g15023300; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTLYHYGVKDLATVFF------YMLVAIIIHATIQEYVLDKLSRRLQLTKGK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 SKGTIQIGTRAIFTLIIVLVALSESLGAENILGAFLAGVLVSLLSPNKELVQQLDSF--- 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 LSSVCSLLYFGDERYQKGLSLW---PIVFISGRLVT----LIVSVVTVG--LHLAGTNRN 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 VSKIIPVMY------LKKWYDNRTIFASGFLLTSTLSLVIAAATIGQQLHVISTN-- 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 ADMVSCVGMF----FVLGLMFEGTAEMSIVFLTLQHGVVVPA---EGLPS---GS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 IILLVAVIADLATMILLAVFSSLYGEDSGNMWILMILFRAGVVLYFFGRVFKHRSFVQSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QNKLNEAGQLSVFYIVSGIWGMI-ILASENCLS---DPTLLWKSQPHNMMTFQMKFFYIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 QLAYWFHSFPELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 107.5; DB 2; Length (20.5%; Pred. No. 0.21; ive 58; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 GNALSGNVNVLAAKIAVLSSSCSIQVY 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 --- MSGALILVAVIASIFTPICFKKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 20.55
Matches 67; Conservative
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A; Status: preliminary
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C;Accession: B83987
R;Takami, H:; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; E
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A)Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06417.1; GSPDB:3-A)Experimental source: strain C-125
C;Genetics: A)Cone: BR5698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABC transporter (permease) BH2698 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                     21;
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                                                                                                                                                                                                                                                     101 TLSAYMF----FSNFYENLFVGVILTAT-----SVSISVQ-TLTELGKLNTRSGINIL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GAYLLYLNHLGLL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 PIDKLTOKFKPOK-----GLAIFSIAAALICAFTAEKLGIAAITGAYI-----CGLV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIMLHY-----AVELLS-SVCSLLYF---GDERYQKGLSLWPIVFISGRLVTLIVSVVT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGLHLAGTNRN-----VLSSSCSIQVYIT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 VIGKILGCSASALTLKFKKSEALQIGVGMVSRGEVAIITANIGLQAKIISEEIFLPTLIV 363
                                                                                                                                                                                                                                                                                                                                        SRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQLSVF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                              --YIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYI-----SQLAYWFHSF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 LSHGIFWKQRKKEF----CLFLSLGMSYQDMVKLMLLENAGIAFLSL------VVGLLS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 GS-----RILYHYGVKDLATVF---FYMLVAIIIHATIQEYVLDKLSRRLQLTKG-- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----KQNKLNEAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----- LVFLY 215
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                  -VFLTLQHGVVVPAEGLPSG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 LSHE-FWVQNHADMVSCVGMFFVLGLMFEGTAEM-----SIVFLTLQHGVVVPAEGLPS 66
                                                                                                                                                     Indels 111;
                                                                                            Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 522;
C;Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :99
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                                                                                            DB 2;
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                                                                                      5.5%; Score 103.5; DE 22.4%; Pred. No. 0.28; ative 59; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.4%; Score 102.5; D 23.2%; Pred. No. 0.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-ELYFQKVRKQDIPGQLIYIGLHLFHIG----
                                                                                                                                                                                                                  19 MVQNHAD--MVSCVGMFFVLGLMFEGTAEMSI-
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29;

89;

Length 360; Indels

DB 2;

KLNEAGQLSVFYIVSG 132

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182 KD--SWLMFVH-HFIALGLLFLSYVDNFTLPGALVLFLHDNSDATLEITKLSFYLKKRTN 238
                                                                                                                                                                                                                                                                                                                                                                                                                133 IWGMIILASENCLSDPTLL---WKSQPHNMMTFQMKFFYISQLAYWFHSFPELYFQKVRK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDIPGQLIYIGLHLFHIGGAYLLYLNHL---GLLLLMLHYAVELLSSVCSLLYFGDERYQ 246
                                                                                                                                                                                                                                                                                                                              6 LYTVLILASIFTFLRYYLQIRLESWTQQHNIYPRFAHKVPESFWKLTYYGTVWIF----A 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYFHMCVDSHDIFNDPLSAMIEWESGGRPKMHWQVQVIYAVQSAFYIHSIYATLFMDLWR 181
                                                                                                                                                                          ; Pred. No. 0.46; 46; Mismatches
   A; Map position: 1
A; Introns: 24/3; 58/1; 88/3; 143/1; 205/2; 310/3
                                                                                                                                      5.3%; Score 100.5; 20.0%; Pred. No. 0.4
                                                                                                                                                                                                                                                                             87 LVAIIIHATIQEYVLDKLSRRLQLTKGKQN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 KGLSLWPIVFISGRLVTLIVSVVTV 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : : ::: | : R--QYYKYYFLMGNAAFILFAIIWV 261
                                                                                                                                                                          Best_Local Similarity 20.0%
Matches 41; Conservative
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NLA 391
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Best Local Si
Matches 64;
                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F13B4.7 - Arabidopsis thaliana
hypothetical protein F13B4.7 - Arabidopsis thaliana
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiAccession: H86286
B;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
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A;Title: Sequence and analysis of Chromosome i of the plant Arabidopsis.
A;Accession: H86268
A;Actatis: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Y6B3B.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27324
R;White, S.
Bubmitted to the EMBL Data Library, October 1998
A;Reference number: 220345
A;Accession: T27324
A;Accession: T27324
A;Accession: T27324
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A;Cross-references: GB:AE005172; NID:99802756; PIDN:AAF99825.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
169 ISQLAYWFHSFPEL--YFQKVRKQDIPGQ--LIYIGLHLFHIGGAYLLYLNHLGLLLLIML 224
                                                                   -----LALSQLGSFLIQM 255
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                                                                                                                                                                             225 HYAVELLSSVC--SLLYFGDERYQKGLSLWPIVFISGRLVTLIVSVVTV 271
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                                                                   216 VMAI----DQYPDMDGYF-----LLGSTVVLFIGLY
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54; Conservative 43; Mismatches 109;
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C;Superfamily: tyrosine-specific transport protein
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us-09-807-470-2.rpr

Search completed: September 6, 2002, 17:11:51 Job time: 6790 sec

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Kidney;
MEDLINE-92244357; PubMed=1315422;
Goerlich D., Hartmann E., Prehn S., Rapoport T.A.;
A protein of the endoplasmic reticulum involved early in polypeptide translocation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Glycoprotein; Translocation
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TRAM protein (Translocating chain-associating membrane protein).
Canis familiaris (Dog).
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (PROBABLE).
1D85808E10806835 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 357:47-52(1992).

-i-FUNCTION: STIMULATORY OR REQUIRED FOR THE TRANSLOCATION SECRETORY PROTEINS ACROSS THE ER MEMBRANE.

-i-SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.

-i-SIMILARITY: BELONGS TO THE LASSI FAMILY.
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LUMENAL (POTENTIAL)
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CFTR_SHEEP
SECY_RICPR
COX1_HIPAM
YDFG_SCHPO
COX1_SHEEP
NKX3_HUMAN
CNT1_HUMAN
                                                                                                                  COX1_CHICK
RFBX_SALTI
COX1_PIG
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PIR; S21736; S21736.
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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125
97.5
96.5
96.5
94.5
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                                                                                                                                                         Perfect score:
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8888880000001
                                                               OM protein
                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                       Searched:
                                                                                         on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
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X63679; CAA45218.1; -. BC000687; AAH00687.1; -.
                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 218; Conserv
                   605190; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Fragment).
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                                                                                          DOMAIN
TRANSMEM
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TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                   Query Match
                                                   DOMAIN
                                                                                                                                  DOMAIN
                                                                     DOMAIN
                                                                                                                                                      DOMAIN
EMBL;
EMBL;
                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9GKZ4;
                                                                                                                                                                                                                                                                                                                                                 62
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                                                                                                                                                                                                                                                                                                                             В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    DERYQKGLSLWPIVFISGRLVTLIVSVVTVGLHLA-GTNRNGNALSGNVNVLAAKIAVLS 300
                                                                                              EGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLFKGKQNKLNEA 121
                                                                                                         | : | :||:||:||:||||||||||:|||:|||:||: EEQATESTSLYYGIKDLATVEFYMLVAIIIHAIIQEYVLDKINRAHFSKTKHSKFNES 121
                                                                                                                                     122 GQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNNMTFQMKFFYISQLAYWFHSFPE 181
                                                                                                                                                 LYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLYFG 241
                                                                                                                                                                                        SSCSIQVYITWTLTTVWLQRWLEDANLHVCGRKRR-----SRSRKGTENGVE---NPNR 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-92244357; PubMed-1315422;
Goerlich D., Hartmann E., Prehn S., Rapoport T.A.;
"A protein of the endoplasmic reticulum involved early in polypeptide
                                     Gaps
                                                                                                                                                                                                                                                                           61
                                                    3 LRKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLĞLMFEGTAEMSIVFLTLQHGVVVPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                           16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
TRAM protein (Translocating chain-associating membrane protein).
                                      11;
                  Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                 DB 1;
                 Score 1145.5; DB Pred. No. 2.7e-88
                                                                                                                                                                                                                                                                                                                                                                           373 AA.
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                   58;
             60.5%;
                                   222; Conservative
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 357:47-52(1992).
                                                                                                                                                                                                                                                                                                    352 IDSPPKKKEKA 362
                                                                                                                                                                                                                                                                                                                         362 ADSPRNRKEKS 372
                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translocation.
                                                                                                                                                                                                                                                                                                                                                                          TRAM_HUMAN
Q15629;
              Query Match
                                   Matches
                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                TRAM_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                      TRAM.
                                                                                                                  62
                                                                                                                                                         122
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241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 DERYQKGLSLWPIVFISGRLVTLIVSVVTVGLHLA-GTNRNGNALSGNVNVLAAKIAVLS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 SSCSIQVYITWTLTTVWLQRWLEDANLHVCGRKRR-----SRSRKGTENGVE---NPNR 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                         61
     Glycoprotein; Translocation.
                                                                                                                                                                                                                                                                                                                                                                                      3 LRKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 LYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Sukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane protein)
                                                                                                                                                                                                                                                              (PROBABLE)
                                                                                                                                                                                                                                                                                                                   Length 373;
                                                                                                                                                                                                                                                                                                                                              81; Indels
                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLONAC. ..) (P);
C220949AF4EFEDDO CRC64;
                                                                    POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                LUMENAL (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                   Score 1129.5; DB 1;
Pred. No. 5.8e-87;
                                                                                                            LUMENAL (POTENTIAL).
                                                                                                                                                                                                                      (POTENTIAL).
                                          POTENTIAL.
LUMENAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TRAM protein (Translocating chain-associating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 AA
                                                                                                                                                                                                                                                                                                                                             61; Mismatches
                  SIMILARITY
                                                                                                POTENTIAL.
                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                          POTENTIAL.
                                                                                                                           POTENTIAL
  Transmembrane;
                                                                                                                                                                                                                        LUMENAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 40, Created)
                                                                                                                                                                                                                                                                           42940 MW;
                                                                                                                                                                                                                                                                                                                 59.7%;
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
Endoplasmic reticulum;
                             28
49
49
75
120
1120
1141
1158
1179
1191
2212
2317
250
2271
2296
3317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 ADSPRNKKEKS 372
                                                                                                                                                 192
213
217
217
272
272
297
318
55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSGSRTL-YHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 RYQKGLSLWPIVFISGRLVTLIVSVVTVGLHLAG-TNRNGNALSGNVNVLAAKIAVLSSS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 KKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPAEGL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSFPELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLLMLHYAVELLSSVCSLLYFGDE
                                                                                                                                                                                                                                                                  Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S., Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.; Prediction of the coding sequences of unidentified human genes. The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced hanalysis of cDNA clones from human cell line KG-I."; DNA Res. 1:223-229(1994).
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE LASSI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.9%; Score 754; DB 1; Length 370; 42.4%; Pred. No. 1.1e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9B5183F1A3D45366 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 132;
                                                                            (Rel. 40, Last sequence update) (Rel. 40, Last annotation update)
                                370 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane
                                PRT;
                                                                                                                                                                                                                                          TISSUE=Bone marrow;
MEDLINE=96051398; PubMed=7584044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                               (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW.
                                                                                                             Hypothetical protein KIAA0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D31762; BAA06540.1; -. EMBL; AL049611; CAB71119.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
160
199
251
288
370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL049611;
Hypothetical pro
                                                               16-0CT-2001
                                                                            16-0CT-2001
16-0CT-2001
                                Y557_HUMAN
Q15035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
SEQUENCE
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                            KIAA0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local
                                                                                                                                                                                                                                                                                                                                                                                                   Tracey
                  7557_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 MIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSFPELYFQKVRKQDIPGQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLYFGDERYQKGLSLWPIV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LVYIGLYLFHIAGAYLLNLNHLGLVLLVLHYFVEFLFHISRLFYFSDEKYQKGFSLWAVL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 VKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQLSVFYIVSGIWG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 FISGRLVTLIVSVVTVGLHLA-GTNRNGNALSGNVNVLAAKIAVLSSSCSIQVYITWTLT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 EFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPA-EGLPSGSRTLYHYG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 NFQLRRWREHSAFQAPAVKKKPPVTKGRSXXKGTENGVNGTVTSNGADSPRNRKEKS 357
                                                                                                                                                                                                                                                                                                                                Transmembrane; Glycoprotein; Translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 TVWLQRWLEDANLHVCGRKR-----RSRS-RKGTENGVE---NPNRIDSPPKKKEKA
                                            (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (Pl
25CF9930C4CDDA15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                             LUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .1e-83;
                                                                                                                                           similarity).
SIMILARITY: BELONGS TO THE LASS1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.3%; Score 1084.5; 59.9%; Pred. No. 3.1e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41403
                                                                                                                                                                                                                                                                                                              EMBL; U19578; AAG10391.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                               reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 AA;
                                FROM N.A.
*CBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S:
Matches 214,
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P28496;
    CONFLICT
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                                ----SRSRKGTENGVENPN 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=S288C / AB972;
MEDLINE=94378003; PubMed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Johnston M., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis B.J., Macri C., Mardis B., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: INVOLVED IN THE AGING PROCESS. DELETION OF LAGI RESULTS IN A PRONOUNCED INCREASE (APPROXIMATELY 50%) IN MEAN AND IN
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94253121; PubMed-8195187; D'Mello N.P., Childress A.M., Franklin D.S., Kale S.D., Pinswasdi C., Jazwinski S.M.; Pinswasdi C., Jazwinski S.M.; "Cloning and characterization of LAG1, a longevity-assurance gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
240 NNEKLFSAWAAVFGVTRLFILTLAVLAIGFGLARMENQAFDPEKGNFNTLFCRLCVLLLV
                                                        300 CAAQAWLMWRFIHSQLRHWREYWNEQ -- SAKRRVPATPRLPARLIKRESGYHENGVVKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO THE LASS1 FAMILY.
                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetáceae; Saccharomyces.
                                                                                                                                                                                                                             UL-FEB-1995 (Rel. 31, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Longevity-assurance protein 1 (Longevity assurance factor 1).
LAGI OR YHL003C.
                                                                                                                                                                                            411 AA
                             303 CSIQVYITWTLTTVWLQRWLEDANLHVCGRKRR-
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                                                                                                                                                                                                                     (Rel. 31, Created)
(Rel. 31, Last seq:
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U08133; AAA21579.1; -. EMBL; U10555; AAB68429.1; -. PIR; S46800; S46800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 265:2077-2082(1994)
                                                                                                                                                                                           STANDARD;
                                                                                                        || || || || 358 NGTSPRTKKLKSP 370
                                                                                      351 RIDSPPKKKEKAP 363
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                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=X2180-1A;
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135
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01-FEB-1995
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P38703;
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                F \; -> \; C \; \; (\text{IN REF. 2}) \, . VFTPFVFGLFVFFWIXLRHVVNIRILWSVLTEFRHEGNYVL
                                                   NFATQQYKCWISLPIVFVLIAALQLVNLYWLFLILKRILYRL
IWQGIQKDERSDSDSSAENEESKEKCE -> TEISGIWE
                                                                                    KQEIDSNDNPTERALSPNETSKQVKPDLLVVLNPTENRNAL
LEAIKSRVPTIAIIDTDSEPSLVTYPIPGNDDSLRSVNFLL
                                                                                                                                                                                                                                                                                                                                   86 MLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQLSVFYI-VSGIWGMIIL-ASEN 143
                                                                                                                                                                                                                                                                                                                                                                    140 MIFFTFLREFLMDVVIRPFTVYLNVTSEHROKRMLEOMYAIFYCGVSGPFGLYIMYHSDL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 L-----YFQKVRKQDIPGQLIYI------GLHLFH 205
                                                                                                                                                                                                                                                                                                91 LVCVYSAYFLSGNRTESNPLHMFVAISYQ-----VDGTDS----YAKGIKDLSFVFFY 139
                                                                                                                                                                                                                                                                                                                                                                                                         -----FHSFPE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLYFGDERYQKGLSLWPIVFISGRLVTLI 265
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MEDLINE-92255906; PubMed-8488728;
BOYER J., Pascolo S., Richard G.F., Dujon B.;
Sequence of a 7.8 kb segment on the left arm of yeast chromosome XI reveals four open reading frames, including the CAPI gene, an introncontaining gene and a gene encoding a homolog to the mammallan UGG-1
                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                             26 MVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPAEGLPSGSRTLYHYGVKDLATVFFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 LLLIWSSYVFHFTKM-----GLAIYITMDVSDFFLSLSKTLNYLNSVFTPFVFGLFVF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                89;
                                                                                                                       GVLARAGQRGLQNRLARNNEK (IN REF. 1)
                                                                                                                                                                                           7.8%; Score 148.5; DB 1; Length 411; 22.0%; Pred. No. 3.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 49.0 kDa protein in UFD4-CAP1 intergenic region.
                                                                                                                                                                                                                                Indels
                                                                                                                                           91676D56AC053F3C CRC64;
   -> IV (IN REF. 2).
                                                                                                                                                                                                                              Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 AA
                                                                                                                                                                                                                                                                                                                                                                                                       144 CLSDPTLLWKSQPHNMMTFQMKFFYISQLAYW----
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                                                                                                                                           MM;
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                                                                                                                                           48454
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
174
220
411
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                                                                                                                                           411 AA;
                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 VSVVTVGLH 274
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173
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301
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          between the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropaen Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in o way
modified and this statement is not removed. Usage by and for commercial
                                                        tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                               GSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQLSV 126
                                                                                                                                                                                                                                                                                                                                121 GDINAYGKGINDLCFVFYYMIFFTFLREFLMDVVIRPFAIRLHVTSKHRIKRIMEQMYAI 180
                                                                                                                                                                                                                                                                                                                                                                                 181 FYTGVSGPFGIYCMYHSDLWFFNTKAMYRTYPDFTNPFLFKVFYLGQAAFWAQQACILVL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 LDSGLAFFSFAIFVVAWIYLRHYINLKILWSVLTQFRTEGNYVLNFATQQYKCWISL-PI 356
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    241 QLEKPRKDHNELTFHHIVTLLIMSSYVFHFTKMGLP---IYITMDVSDFLLSFSKTLNY
                                                                                                                                                                                                                                                                                                                                                            FYI-VSGIWGMIIL-ASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYW-----
                                                                                                                                                                                                                                                                                                                                                                                                       -----FHSFPEL----YFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 L--GLL------LLMLHYA-VELLSSVCS------LLYFGDERYQKGLSLWPI
                                                                                                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                                                  Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyne M., Wood V., Rajandream M.A., Barrell B.G., Brown D.,
Churcher C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 42.4 kba protein C3E17.15c in chromosome II.
SPBC3E7.15C OR SPBC4F6.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Churcher C.M.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                     POTENTIAL. 7691BA623AC0460A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                 7.2%; Score 137; DB 1;
23.5%; Pred. No. 0.00034;
tive 44; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 AA
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                                                                                       EMBL; X61398; CAA43670.1; -. EMBL; S59773; AAC60549.1; -. EMBL; Z28008; CAA81843.1; -.
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                                                                                                                          PIR; S30134; S30134.
SGD; S0001491; YKL008C.
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260
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418 AA;
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16-0CT-2001 (
16-0CT-2001 (
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                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 VAIIIHATIQEYVLDKLSRRLQL-TKGKQNKLNEAGQLSVFYIVSGIWGMIIL-ASENCL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 FFTFCREFIMQEIIARIGRHFNIRAPAKLRRFEEQAYTCLYFTVMGSWGLYVMKQTPWWF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 SDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSFPELYFQ--KVRKQDIPGQLIYIGLHL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 EGTAEMSIVFLTL-------QHGVVVPAEGLPSGSRTLYHYGVKDLATVFFYML 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 FNTDAFWEEYPHFYHVGSFKAFYLLEAAYWIQQALVLILQLEKPRK-DFKELVVHHIITL
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01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Longevity-assurance frotein 1 (Longevity assurance factor 1).
LAGI OR SPACIA6.09C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 133; DB 1; Length 38 Pred. No. 0.00067; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chanda E.R., Lingner C., Ko Z., Young P.G.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82FCF8EA6638849A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
SIMILARITY: BELONGS TO THE LASSI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 AA.
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                  EMBL, AL023534; CAA19018.2; -.
EMBL; AL031534; CAA20722.2; -.
Hypothetical protein; Transmeml
TRANSMEM 59 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45335 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.5%;
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Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bartoloni L., Wattenhofer M., Kudoh J., Kawasaki K., Rossier C., Shimizu N., Scott H.S., Antonarakis S.E.; "Identification and characterization of the human glycerol 3-phosphate permease gene (SLC37A1) mapping to 1q22.3; expression pattern, genomic structure and cDNA sequence."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                             65 PSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQN----KLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 PDGS---YGKGPKDACFPIFWVIVFTAFRVIVMDYVF----RPFVLNWGVRNRKVIIRFC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 EAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 EQGYSFFYYLCFWFLGLYIYRSSNYWSNEEKLFEDYPQYYMSPLFKAYYLIQLGFWLQQI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 PELYFQKVRKQD-----IPGQLIYI--GLHLFHIGGAYLLYLNHLGLLLL----ML 224
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 LVLHLEQ-RRADHWOMFAHHIVTCALIILSYGFNFLRVGNA-ILYIFDLSDYILSGGKML 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Solans A., Estivill X., de la Luna S.; "Cloning and characterization of human glycerol 3-phosphate permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 HYAVELLSSVCSLLYFGDERYQKGLSLWPIVFISGRLVTLIVSVVTV-----GLHL 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 KYLG--FGKICDYLF-----GIFVASWVYSRHYLFSKILRVVVTNAPEIIGGFHL 322
                                                                                                                                                                                                                                                                                             EDEEASSTNEDK -> GRRGGEFNE (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene (SLC37A1).";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE SLC37A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                    46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLPT_HUMAN STANDARD; PRT; 533 AA.
P57057; Q9HAQ1;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycerol-3-phosphate transporter (G-3-P transporter) (G-3-P
                                                                                                                                                                                                                                                                                                                                                           6.6%; Score 125; DB 1; Length 390; 23.9%; Pred. No. 0.0032; tive 35; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                             DC00FB5C2D2F22CC CRC64;
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                                                                                                  EMBL; U76608; AAB19113.1; -. EMBL; Z99258; CAB16359.1; -.
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83
137
175
219
251
251
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                                                                                                                                                                                                                                                                                                         390 AA;
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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SEQUENCE FROM N.A.
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63
117
155
199
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                                                                                                                                     Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                               57;
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GLPT_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GLPSGSRTLYHYGVKDLATVFFYMLV------AIIIHATIQEYVLDKLSRRLQLTK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 NAMTFQMKFFYISQLAYWFHSFPELYFQKVRKQDI--PGQLIYIGLHLFHIGGAYLLYLN 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - GGILAGVISDRLEKRASTCGLMLLLAAPTLYIFSTISKMGLEATIAMLLLSGALVSGPY 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VLGLMFEG---TAEMSIVFLTLQHGVVVPAE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 GI-------VCFLFLIEHPNDVRCSSTLVTHSKGYENGTNRLRLQKQILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 GKQNK------LNEA-GQLSVFYIV----SGIWGMIILASENCLSDPTLLWKSQPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 SEKNKPLDPEMOCLLLSDGKGSIHPNHVVILPGDGGSGTAAISFTGALKIP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 HLGLLLLMLHYAVELLSSVCSL-----LYFGDERYQKGL-SLWPIVFISGRLV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    %10-FEB-1994 (Rel. 28, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
02-Stic fibrosis transmembrane conductance regulator (CFTR) (cAMP-dependent chloride channel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 533;
                                                                                                                                                                                                                                                                                                                                                                   -> L (IN REF. 2).
-> Q (IN REF. 2).
EA888FE2942380A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 TLIVSVVTVGLHLAGTNRNGNALSGNVNVLAAKIAVLSSSCSI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1450 AA
                                                                                                                                                                                             Transport; Sugar transport. 38 POTENTIAL.
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                                                                                                                                                               InterPro; IPR000849; GlpT_transporter.
PROSITE; PS00942; GLPT; FALSE_NEG.
                                                                                                                            AJ277912; CAB91985.1; -. AJ277913; CAB91986.1; -.
                                                                                                                 EMBL; AJ269529; CAB87248.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
                                                                                                                                                      AF311320; AAG29853.1;
                                                                                                                                                                                                                                                                                                                                                                                             57662
                                                                                                                                                                                                                                                                                                                                                                                                                                                            69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 MVSCVGMFF-----
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149
177
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4443
486
510
5223
303
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303
533 AA;
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Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                              Transmembrane;
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Q00554;
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1010 LKQLESEGRSPIFTHLVTSLKGLWTLRA-----FGRQPY----FETLFHKALNLH 1055

116 NK-LNEAGQLSVF-YIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQL-

893 ADTLLALGLFRGLPLVHTLITVSKILHHKMLHSVL---QAPMSTLNTLKAGGILNRFSKD 949

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                                                                                                                                                                                                                                                                   'Cystic fibrosis gene encodes a cAMP-dependent chloride channel in
                                                                                                                                                                                               MEDLINE-92042228; PubMed-1719001; Dalamond G., Scanlin T.F., Zasloff M.A., Bevins C.L.; Dalamond G., Scanlin T.F., Zasloff M.A., Bevins C.L.; A cross species analysis of the cystic fibrosis transmembrane conductance regulator. Potential functional domains and regulatory
Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                     TISSUE-Heart ventricle;
MEDINE-96270540; PubMed-8692817;
Hart P.H., Warth J.D., Levesque P.C., Collier M.L., Geary Y.,
Horowitz B., Hume J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART: SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Transmembrane; Transport; Glycoprotein; Repeat; Ionic channel; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAFFF5838B5D20EE CRC64;
                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 93:6343-6348(1996).
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5 (POTENTIAL).
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(POTENTIAL).
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Interpro; IPR00140; ABC_transporter_tmem.
Interpro; IPR00140; ABC_transportr.
Interpro; IPR001587; APC_Transportr.
Pfam: PF00664; ABC_membrane; 2.
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                                                                                                                                                                                  SEQUENCE OF 574-745 FROM N.A.
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HSSP; P13569; 1NBD.
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1450 AA;
                                                        SEQUENCE FROM N.A.
                            NCBI_TaxID=9986;
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1214
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-I FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHALVESS THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSPERRED VIA THE COPPER A CENTER FORMED BY HEME AS AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME AS AND COPPER B (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                          1168 VKKDDVWP----SGGQMTVKGLTAKYIDSGNAILENISFSISPGQRVGLLGRTG---SGK 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBCELLULAR LOCATION: Integral membrane protein.
                          1108 NIMSTLOWAVNSSIDVDSLMQSVSRVFMFIDMPTEAKSTKSIKPSSNCQLSKVMIIENQH 1167
                                                                            245
                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable cytochrome c oxidase polypeptide I (EC 1.9.3.1) (Cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sicheritz T., Kurland C.G., Andersson S.G.E.; "The bacterial origin of mitochondria inferred from a phylogenetic analysis of the cytochrome b and cytochrome c oxidase I genes."; submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-MADRID E;
MEDLINE-299139499;
Andersson S.G.E., Zonorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Inhe genome sequence of Rickettsia prowazekii and the origin of
mitochondria."
                                                                                                                                                        246 QKGLSLWPIVFISGRLVTL-------IVSVVTVGLHLAGTNRNGNALSGN
                                                                              ----LHYAV-----ELLSSVCSLLYFGD-----------ERY
173 -AYWFHSFPELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYL-----NHLGLLLLM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : TERMINAL STEP IN THE RESPIRATORY CHAIN.
                                                                                                                                                                                                                                                        534 AA
                                                                                                                                                                                                                                  289 VNVLAAKIAVLSSSCSIQV-YITWTLTTVWLQRW 321
                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, 30-MAY-2000 (Rel. 39, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTAD OR COXA OR RP405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=782;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA3 subunit
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054069;
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22;

Gaps

24 ADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPAEGLPSGSRTLYHYGV-----KD 78

21.3%; Pred. No. 3.2; ative 62; Mismatches 118; Indels 130;

Conservative

Sest Local Similarity

Query Match

84;

Matches

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5.1%; Score 97; DB 1; Length 1450;

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DD BREET THE THE TENT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT O
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PA------EGLPSGSRTLY-----HYGVKDLATVFFYMLVAIIIHATIQEYVL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 GSINLIVTIFNMRTPG------MGLFKMPLFVWSILVTAFLIILAMPVL---SGAI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NMM----TFQMKFF-----YISQLAYWFHSFPELYF------QKV----RK-- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---QDIPGQLIYIGL------HLFHIGGAY--LLYLNHLGLLLLMLHYAVELLSSVCS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 121; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAFLLLISSTFIDGGPGTGWTLYPPLSNLNGHTGAAVDVAIF-----SLHLTGLSSIL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 DKLSRRLQL----TKGKQNKLNEAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPH 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 FGYQGMYGAMYIIGFYGFIVWAHHMFTYGLSYNALIYFT-AGTMIIAVPTGIKIFSWIA- 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSHEFMVQNHADMVSCVGM--FFVLGLMFEGTAEMSIVFL------TLQHGVVV 59
                                                                                                                                                                                                          PROSITE; PS00077; COX1; 1.
Oxidoreductase; Heme; Copper; Transmembrane; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 96.5; DB 1; Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 LLYFGDERYQKGLSLW------PIVFISGRLVTLIVSVVTVGLHLAGT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRON (HEME A3) (PROBABLE).
IRON (HEME A) (PROBABLE).
326E6B5753548C3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.1%; Score yo., __
18.6%; Pred, No. 1.1;
tive 57; Mismatches 107;
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POTENTIAL.
POTENTIAL.
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                                                                                                                                                                      Pfam; PF00115; COX1; 1.
PRINTS; PR01165; CYCOXIDASEI.
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                                                                                                                         EMBL; AJ235271; CAA14862.1;
                                                                                                                                       4SSP; P98002; 1AR1.
InterPro; IPR000883; COXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59261
                                                                                                         EMBL; Y13855; CAA74167.1;
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395
397
534 AA;
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                                                                                                                                                                                                                                               Complete proteome. TRANSMEM 35
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76
1120
1120
1202
202
202
3320
3320
433
475
811
260
309
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P77175;
16-OCT-2001
16-OCT-2001
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TRANSMEM
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YDIK_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Mimta S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Moromura M., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 VFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQLSVFYIVSGIWGMIILAS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 ENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSFPELYFQKVRKQDIPGQLIYIGL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----IVDGSGPLIKAIS 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 IVACLWIVOPFILGFAWAGTVVIATWPVLLRLOK-----IMFGRRSLAVLVWTLLLV 75
                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-KIZ. / MGIG55;
STRAIN-KIZ. / MGIG55;
Pubbed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 MVSCVGMF--FVLGLMFEGTAEMSI--VFLTLQHGVVVPAEGLPSGSRTLYHYGVKDLAT 81
                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLUIAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corresponding to the 28.0-40.1 min region on the linkage map."; DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000264; AAC74758.1; -.
EMBL; D90811; BAA15450.1; -.
ENGLen; EG13970; ydik.
Interpro; IRR003549; UPP0118.
Pfam; PF01594; UPP0118; 1.
Hypothetical protein; Transmembrane; Complete proteome.
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  40, Last annotation update)
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19.5%; Pred. No. v.-
...a 50; Mismatches
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Pred. No. 0.94;
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                           protein ydiK.
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76 MVFIIPIALLVNS----
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16-OCT-2001 (Rel.
Hypothetical prote
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67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                Escherichia coli
                                                                                                                                                           NCBI_TaxID=562;
                                                    YDIK OR B1688
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(Rel. 40, Created) (Rel. 40, Last sequence update)

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STANDARD;

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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                          "Tissue-specific expression and cholesterol regulation of acylcoenzyme A:cholesterol acyltransferase (ACAT) in mice. Molecular cloning of mouse ACAT CDNA, chromosomal localization, and regulation of ACAT in vivo and in vitro.";
J. Biol. Chem. 270:26192-26201(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homologue of the
                                                                                                                                                                                               061263: 064180;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Sterol O-acyltransferase 1 (EC 2.3.1.26) (Cholesterol acyltransferase
1) (Acyl coenzyme A:cholesterol acyltransferase 1) (ACAT-1).
                                            183
                                                                             ----WLNTIP------VIGAKLYAGW 127
                                                                 245 YQKG--------LALWPIVFIS-GRLVTLIVSVVTVGLHLAGTNRNGNAL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           its potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               !ransferase; Acyltransferase; Transmembrane; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: Acyl-CoA + cholesterol = CoA + cholesterol
                                   202 H-LFHIGGAYLL----YLN------HLGLLLIMLHYAVELLSSVCSLLYFGDER
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reticulum.
SIMILARITY: BELONGS TO THE STEROL O-ACYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                          MEDIINE-96064687; PubMed-7592824;
Uelmen P.J., Oka K., Sullivan M.C., Chang T.-Y., Chang C.C.Y.,
                                                                                                                                  SG-VPYATLLTVLMILSCLVQLGPLPVLIPAIIWLYWTGDTTW 277
                                                                                                           286 SGNVNVLAAKIAVLSSSCSIQ------VYITWTLTTVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L42293; AAC42075.1; -.
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InterPro; IPR002688; ACAT.
Pfam; PF01800; ACAT; 1.
                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cholesterol metabolism.
                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
102 SGDMTLPDLA--
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                  IISSUE-Liver
                                                                                                                                                                                         SOA1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A second terminal oxidase in Sulfolobus acidocaldarius.";
Eur. J. Blochem. 224.151-159(1994).
-!- FUNCTION: TERMINAL OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SOXM
FORMS THE FUNCTIONAL CORE OF THE ENZYME COMPLEX.
-!- FUNCTION: CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING
IN A QUINOL ARE TRANSFERRED TO THE BIMETALLIC CENTER OF SOXM
FORMED BY A HEME AND COPPER B.
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: TWO HEME GROUPS AND COPPER B.
-!- PATHWAY: TERRINIAL STEP IN THE RESPIRATORY CHAIN.
-!- FATHWAY: TERRINIAL STEP IN THE RESPIRATORY CHAIN.
-!- SUBUNIT: FORMS A COMPLEX WITH AT LEAST SOXC AND A 30 KDA RIESKE
FE-S PROTEIN, BUT NEITHER WITH SOXA NOR SOXB.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- FTM: SOXM IS PROABBLY A PRECURSOR FORM OF SUBUNITS I AND III.
-!- SIMILARITY: IN THE N-TERRINAL SECTION; BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                         IVFLTLQHGV-----VVPAEGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                     101 LDKLSRRLQLTKGKQNK--LNEAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 RENIPRVLNAAKEKSSKDPLPTVNQYLYF----LFAPTLIYRDNYPRTPTVRW---GYV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMTFQMKFFYISQLAYWFHSFPELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 LLFLVFQLGVLGFVPTYVVLAYTLPPASR-------FILLLEQIRLIMKAHSFV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luebben M., Arnaud S., Castresana J., Warne A., Albracht S.P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                Length 540;
                                                                            POTENTIAL.
P -> R (IN REF. 2).
8EF900C8BCDF73C0 CRC64;
                                                                                                                                                                                                                  DB 1;
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01-FEB-1995 (Rel. 31, Last sequence update)
01-WAY-2000 (Rel. 39, Last annotation update)
011nol oxidase polypeptide I/III (EC 1.9.3.-)
                                                                                                                                                                                                                                               1.6;
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                                                                                                                                                                                                                                                                   34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 33909 / NCIB 11770 / DSM 639;
MEDLINE-94357214; PubMed-8076636;
                                                                                                                                                                                                                  Score 94.5;
Pred. No. 1.
                                                      POTENTIAL.
POTENTIAL
                            POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 LLLLMLHYAVELLSSVCSLLYFGDERYOK
                                                                                                                                      63739 MW;
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                                                                                                                                                                                                                                                                         Conservative
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331
372
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540 AA;
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ID ATP6_BUCAP
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 GLPS------GSRTLYHYGVKDLATVFFYMLVAIIIHATIQE------YVLDKLSR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                 134 ETTVNYGLGTNL----IQIALILSGLSSTLTGVNFVMTITKMKKVPYLKMPLFVWGFFT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LASENCLSDPTLLWKSQPHNMMTFQMKFFYISQL--------AYWFHSF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MLHYAVELLSSVCSL------LYFGDERYQKGLSL---WPIVFISGRLVT 263
                                                                                                                                                                                                                                                                                                                                                   98; Indels 147; Gaps
                                                                                                                                                                                                                                                                                                                                                                   28 SCVG-MFFVLGL--MFEGTAEMSIV----FLTLQ-------HG-----VVVP-AE 62
                                                                                                                                                                                                                                                                                                                                                                              189 TAILMIIAMPSL-----TAGLVFAYLERLWGTPFFDSALGGSPVLWQQLFWFFGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Respiratory chain.
                                                                                                                                                                                                                                                                                                                                   5.0%; Score 94.5; DB 1; Length 788; 19.5%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                             IRON (HEME A(3)) (PROBABLE).
IRON (HEME A) (PROBABLE).
3939C16CDB8A08AD CRC64;
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IRON (HEME A) (PROBABLE).
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                                    InterPro; IPR000883; COX1.
InterPro; IPR000298; CytC_oxdse_III.
Pfam; PF00115; COX1; 1.
Pfam; PF00510; COX3; 1.
                                                                                                                                                                                                                                                                               COPPER
                                                                                                                                                                                                                                                                                       COPPER
                                                                                                                                                                                                                                                                                                                                                   57;
                                                                                             Copper;
                                                                    PRINTS; PRO1165; CYCOXIDASEI. PROSITE; PSO0077; COX1; 1. PROSITE; PS50253; COX3; 1.
                                                                                                                                                                                                                                                                                                             87082 MW;
                      EMBL; X73567; CAA51969.1; -.
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 LIVSVVTVGLHLAGT 278
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                                                                                             неше;
                                                                                                                                                                                                                                                                                                             88 AA;
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                             Oxidoreductase;
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657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC SUBUNIT: F-TYPE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 HYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQLSVFYIVSG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 IWGMIILASENCLSDP----TLLWKSQPHNMMTFQMKFF-YISQLAYWFHSFPELYFQKV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 HFWVLNIDSIIFSLVLGCFFLSIF--YTVAK-----KITTGVPNGLQASIELIFDFIRSN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark M.A., Baumann L., Baumann P.; "Sequence analysis of a 34.7-kb DNA segment from the genome of sequence analysis of a 34.7-kb DNA segment from the genome of buchnera aphidicola (endosymbiont of aphids) containing gro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 VKSM--YQGKNPLIAPLSLTVFVWVFLMNLMDLIPIDFFPFISE--RFFH-FPAM-----
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=97361981; PubMed=9216881;
Clark M.A., Baumann P.;
The (FIFO) ATP synthase of Buchnera aphidicola (endosymbiont of aphids); genetic analysis of the putative ATP operon.";
Curr. Microbiol. 35:84-89(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87; Indels
                                                                                                                                                                                                                          Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCD8C7D2C98C37CC CRC64;
                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MXZ-2000 (Rel. 39, Last annotation update)
ATP synthase A chain (EC 3.6.3.14) (Protein 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrogen ion transport; CF(0); Transmembrane.
TRANSMEM 41 61
272 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=98184963; PubMed=9516544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P00855; 1C17.
InterPro; IPR000568; ATP_synt_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF008210; AAC38116.1; -.
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272 AA;
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                                                                                                                                                                                                                                                                                     NCBI_TaxID=98794;
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Search completed: September 6, 2002, 17:21: Job time: 632 sec V

Q91jk3 arabidopsis Q9m6a2 arabidopsis 096g23 homo sapien

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0992424 must suppression of partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial partial pa
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGLRKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 59.5%; Score 1125.5; DB 11; Length 374; Best Local Similarity 58.4%; Pred. No. 5.6e-93; Matches 218; Conservative 58; Mismatches 86; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AYO29764; AAK38167.1; -.
EMBL; BC012401; AAH12401.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43039 MW; E6C65250F68E4393 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                091V04;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotati
TRAMI (UNKNOWN) (PROTEIN FOR MGC:11724).
MUS musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; V
09LJK3
096A2
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0924Z4
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091DF2
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O9w5c3 drosophila
O9u113 drosophila
O9u3p5 caenorhabdi
O9xxX7 caenorhabdi
O9cyf6 mus musculu
Q9d6j1 mus musculu
Q9ha82 homo sapien
Q9m6a4 lycopersico
Q9fin6 drosophila
                                                                                                                                                                                    (without alignments)
783.105 Million cell updates/sec
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090zl9 xenopus lae
0924z5 mus musculu
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                                                                                                                                                            ; Search time 80.19 Seconds
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                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                      562222 segs, 172994929 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Q902M1
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Q95RN6
Q9CHC2
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Gapop 10.0 , Gapext 0.5
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Match Length
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Total number of

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Q980x8 sulfolobus Q90ze4 brachydanio Q93xx4 arabidopsis

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1102 1024 762 762 762 566 561 441.5 4348 1163.5 1183.5 1119.5

Score

Result

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οy 셤 Qγ 염 δy Db

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Brachydanio rerio (Zebrafish) (Zebra danio).

Makaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                            Query Match

S4.1%; Score 1024; DB 13; Length
Best Local Similarity 52.4%; Pred. No. 7.2e-84;
Matches 193; Conservative 67; Mismatches 102; Indels
                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                           Hartmann E.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ database:
EMBL; AY029529; AAK40297.1; -.
SEQUENCE 369 AA; 41743 MW; A3EE6263E3165846 CRC64;
                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 19,
                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :|||:
361 PRARKEKS 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 PPKKKEKA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001
                                           Q902M1
Q902M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q90ZL9;
Q90ZL9;
                                                                                                                TRAM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
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                RESULT
                               290ZM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                    349
121 ESGQLSAFYLFACVWGTFILISENYISDPTILWRAYPHNLMTFQTKFFYISQLAYWLHAF 180
                                                                                                   61 AEGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSSCSIQVYITWTLTTVWLQRWLEDANLHVCGRKRRSRSRKG-----TENGVE---NPN 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGLRKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGDERYQKGLSLWPIVFISGRLVTLIVSVVTVGLHLA-GTNRNGNALSGNVNVLAAKIAV
                                                                                                                                        LSSSCSIQVYITWTLTTVWLQRWLEDANLHVCGRKRR-----SRSRKGTENGVE---NP
                            180 PELYFOKVRKODIPGOLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSYCSLLY
                                           Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1102; DB 13; Length 373;
Pred. No. 7.2e-91;
4; Mismatches 89; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY029534; AAK40302.1; -.
SEQUENCE 373 AA; 43121 MW; 62AFA9E9859769DF CRC64;
                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                    373 AA.
                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.2%;
56.1%;
                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel 19, 01-DEC-2001 (TrEMBLrel 19, 01-DEC-2001 (TrEMBLrel 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208; Conservative
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                 350 NRIDSPPKKKEKA 362
                                                                                                                                                                                                                    | ||| :|||:
NGADSPRNRKEKS 373
                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIDSPPKKKEK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||| :|||
|GADSPRSRKEK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hartmann E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                               090ZMO;
                                                                                                                                                                                                                                                                                              Q90ZMO
                                                                                                                                                                                                                           361
                                                        181
                                                                                    240
                                                                                                                                          599
                                                                                                                                                                                                                                                                                                                                                                   TRAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
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Length 369;

RESULT Q902M0

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61 AEGLPSGSRTLY-HYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLN 119
                                                                    EAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSF 179
                                                                                                                                                                                                                                                                                                          360
               1 MGLRKKNARNPPVLSHEFMYQNHADMYSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVP
                                                                                                                          PELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLY
                                                                                                                                                                               240 FGDERYQKGLSLWPIVFISGRLVTLIVSVVTVGLHLAGTNRNG-NALSGNVNVLAAKIAV
                                                                                                                                                                                                                                                                       299 LSSSCSIQVYITWTLTTVWLQRWLEDANLHVCGRK---RRSRSRKGT-ENGVENPNRIDS
                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hartmann E.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY029535; AAK40303.1; -.
SEQUENCE 371 AA; 43548 MW; 582231A5286D130B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                             371
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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RAINTH-EBSTRELEY;
RAINTH-EBSTRELEY;
RAINTH-EBSTRELEY;
RAMBER M.D. Celnikrer S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RAMBER M.D., Celnikrer S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RAMBER M.D., Celnikrer S.E., Li P.W., Hoskins R.A., Galle R.E.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RAMEROGO R.C., Wortham J.R., Yandell M.D., Zhang Q., Chen L.X.,
RAMER M. Brandon R.C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,
RAMER M. Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RAMELI J.F., Agbayaria A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RAMER M. Benos P.V., Berman B.P., Bandaril D., Bolshakov S.,
RAMER M. Cavaley S., Dallike C., Davenport L.B., Davies P.,
RAMERIS K.C. Busam D.A., Bulle H., Cadleu E., Center A., Chanfra I.,
RAMER M. Cavaley S., Dallike C., Davenport L.B., Davies P.,
RAMER M.J., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RAMER M.J., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser R.,
RAMER M., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Cabaser R.,
RAMER M., Gong F., Gorrell J.H., Gu Z., Glan P., Harris M.L.,
RALLS K.C., Moyland T.J., Hernandez J.R., Heurtis M.
RAULON E., Kodira C.D., Kraft C., Shanders R., Belact E., Spradlina A.C., Shanders R., Welsenbach J.,
Ray Shue B.C., Siden-Klamos I., Simpson M., Stupski M., Shue B.C., Shan H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Meopiera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
180 FQKVRKEEVPRQLQYICLYLLHITGAYLLNLSRLGLILLLLQYSTEALFHMARLFHFADE 239
                                                        RYQKGLSLWPIVFISGRLVTLIVSVVTVGLHLAGT-NRNGNALSGNVNVLAAKIAVLSSS 302
                                                                                                                                                                                                                                     300 CVAQAWLMWRFIHSQLRHWREYWKEQSAKRRVSAVPRPPAKLLKREPGYHENGVVKAENG 359
                                                                                                                 240 NNERLFNAWAAVFGVTRLFILTLAVLTIGFGLARVENQVFDPEKGNFNTLPCRLGMLLLV
                                                                                                                                                                             303 CSIQVYITWTLTTVWLQRWLE----DANLHVCG-----RKRRSRSRKGTENGVENPNRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003419; AAF45569.1; -.
FlyBase; FBgn0040340; EG:BACR7A4.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY 2000 (TrEMBLrel. 13, 01-MAY 2000 (TrEMBLrel. 13, 01-MAR 2001 (TrEMBLrel. 16, EG:BACR7A4.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                       | || || |:|
360 TSSRTKKLKSP 370
                                                                                                                                                                                                                                                                                              353 DSPPKKKEKAP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 VVVPAEGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQN 116
                                                                                                                                                                                                                                                                                                                              S SSIQT---LDGELLYYHYGVKDLVTILFYVVIAIILHAIVQEYILDKINKRLHLSKVKQS 111
                                                                                                                                                                                                                                                                                                                                                                                                                KLNEAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                               PSGSRTL-YHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEAGQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | |: |||| ||| || |: ||::: || || :|||:|| |:|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |:|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                      1 MGLRKKNARNPPVLSHEFMVQNHADMVSCVGMFFVL----GLMFEGTAEMSIVFLTLQHG 56
                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSFPELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLYFGDERYQKGLSLWPIVFISGRLVTLIVSVVTVGLHLAGTN-RNGNALSGNVNVLAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 IAVLSSSCSIQVYITWTLTTVWLQRWLEDANLHVCGRKRRSRSRKGT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 KKNARNPPVLSHEFWVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPAEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 LSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSFPELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVCSLLYFGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                        Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.4%; Score 727; DB 11; Length 37(40.7%; Pred. No. 3.4e-57;
Live 70; Mismatches 134; Indels
                                                                                                                 Indels
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EMBL; AY029530; AAK40298.1; -
SEQUENCE 370 AA; 43182 MW; F8E768AFB0582548 CRC64;
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Last annotation update)
                                                                                                                 122;
                                                     40.3%; Score 762; DB 13;
41.2%; Pred. No. 2.5e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 AA.
                                                                                 Pred. No. 2.5e
67; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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Best Local Similarity 40.7%
Matches 151; Conservative
                                                                                                              Conservative
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                                                                                 Similarity
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                                                                                                              159;
                                                     Query Match
                                                                                        Local
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Q924Z5;
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Matches
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RA Mannatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Baytaktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delchen A., Deng Z., Mays A.D., Dew I., Ditter S.M.,
RA Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellan A.E., Garg N.S., Glubr F., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Well M.-H., Ibegwam C.,
                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GG18830 PROTEIN.
GG18830 OR GG16994.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                              CSLL--YFGDERYQKGLSLWPIVFISGRLVTLIVSVVTVGLHLAGTNRNGNALSGNVNVL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAKIAVLSSSCSIQVYITWTLTTVWLQRWLEDANLHVCGRKRRSRSRKGTENGVENPNRI 352
                                                                                                                                                                                                                                                                                                                                           EGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSFPE 181
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                                                                                                                                                                                                                 4 RKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGV--VVPA 61
                                                                                                                                                                                                                                                    LYPQKVR-KQDIPGQLIYIGLHLFHIGG-----AYLLYLNHLGLLLLMLHYAVELLSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYPQKIKTKEEQQPKIVH-----SISGFTLIVLAYTLSFORLALVLLTLHYFSELLSHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 FOLIGVFDREERLAKLRVVNNAVFFLIRFATSVIGVLTLYYGIGGV-RSLLALGGLI---
                                                                                                                                                          38;
                                                                                             Length 368;
                                                                                                                                                          Indels
693794394C2ED787 CRC64;
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Last annotation update)
                                                                                          ; Score 566; DB 5; L; Pred. No. 9.9e-43; 64; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1575 AA.
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41780 MW;
                                                                                      29.9%;
ilarity 37.0%;
Conservative 64
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AA;
                                                                                                                   Similarity
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368
                                                                                      Query Match
Best Local Simil
Matches 136; (
SEQUENCE
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A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., McRavito G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Andra M., Mohy M., Murphy B., Murphy L., Murphy D.M., Nelson D.L., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., She B. Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Tatpleton M., Strong R., Sun E., Syrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Re Johog R.H., Zhong F.W., Zhon M., Zhou X., Zhu S., Zha S., Zha S., Zha S., Zhu S., Zhu S., Smith H.O., R., Shong R., Smith B. S., The Genome sequence of Drosophila melanogaster.";
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EG:BACK7A4.5 PROTEIN.
EG:BACK7A4.5 OR CG11642.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Metazoa; Arthropoda; Tracheata; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSFPE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLNEA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 RKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGV--VVPA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1396 LYFQKIKTKEEQQPKIVH-----SISGFTLIVLAYTLSFQRLALVLTTHYFSELLSHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYFQKVR-KQDIPGQLIYIGLHLFHIGG-----AYLLYLNHLGLLLLMLHYAVELLSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 CSLL--YFGDERYQKGLSLWPIVFISGRLVTLIVSVVTVGLHLAGTNRNGNALSGNVNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 AAKIAVLSSSCSIQVYITWTLTTVWLQRWLEDANLHVCGRKRRSRSRKGTENGVENPNRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.9%; Score 566; DB 5; Length 15 37.0%; Pred. No. 5.5e-42; ive 64; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1575 AA; 172376 MW; 2F8C0E528B67CD69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0040340; EG:BACR7A4.5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
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236 SLLYFGDERYQKGLS----LWPIVFISGRLVTLIVSVVT--VGLHLAGTNRNGNALSGN 288
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                                                                                                                                                                               EGLPSGSRTLYHY -- GVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLN 119
                                                                                                                                                                                                    67 AVEQGQEREVHGYLSGILDLPAIFFYSVCWIVVHAVVQEYGLDKISKKTHLSKVSTFKFG 126
                                                                                                                                                                                                                                                       EAGQLSVFYIVSGIWGMIILASENC -- LSDPTLLWKSQP -- HNMMTFQMKFFYISQLAYW 175
                                                                                                                                                                                                                                                                                                                          176 FHSFPELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMLHYAVELLSSVC 235
                                                                                                                                                                                                                                                                                                                                                                                                                       62 EGLPSGSRTLYHY -- GVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTKGKQNKLN 119
                                                                                                           2 GLRKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPA 61
                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GLRKKNARNPPVLSHEFMVQNHADMVSCVGMFFVLGLMFEGTAEMSIVFLTLQHGVVVPA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCMULTAY A.A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         investigating biology.";
Science 282:2012-2018(1998).
EMBL; ALO22716. CAA18772.1; -.
InterPro: IPR001185; MSCL.
SEQUENCE: 373 AA; 42655 MW; 92D65DF05F50B9CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.0%; Score 434.5; DB 5; 30.1%; Pred. No. 6.5e-31; ive 75; Mismatches 151;
                                     23.3%; Score 441.5; DB 30.0%; Pred. No. 1.5e-31
                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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MEDLINE-99069613; Pubmed-9851916;
                                                                       16;
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350 AAAV---PKKEKK
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Best Local Similarity
Matches 113; Conserv
                                                      Similarity
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                                                      Local Simples 112;
                                       Query Match
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                                                        Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 GQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMKFFYISQLAYWFHSFPE 181
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 LYFQKVR-KQDIPGQLIYIGLHLFHIGG-----AYLLYLNHLGLLLLMLHYAVELLSSV
SEQUENCE FROM N.A.

spapismentis G., Spanos L., Bolshakov V., Siden-Kiamos I., Louis
"Sequencing the distal X chromosome of Drosophila melanogaster.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                      Length 368;
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                                                                                                                                                                                                                                  Query Match 29.7%; Score 561; DB 5; Length 36 Best Local Similarity 36.7%; Pred. No. 2.8e-42; Matches 135; Conservative 64; Mismatches 131; Indels
                                                                                                           Benos P.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                     EMBL, AL109630, CAB65875.1;
Flybase; FBgn0040340; EG:BACR7A4.5.
SEQUENCE 368 AA; 41766 MW; 693795FFFC2ED4A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998).
EMBL: ALO22716. CANABT70.1; -.
InterPro: IPR001185; MSCL.
SEQUENCE 371 AA; 42420 MW; 5269FC7231222592 CRC64;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Submitted (APR-1998)
                                                                                      SEQUENCE FROM N.A.
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Indels

Length 373;

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PRELIMINARY;

Created) PRT;

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275 LA-GTNRNGNALSGNVNVLAAKIAVLSSSCSIQVYITWTLTTVWLQRWLEDANLHVCGRK 333
                                                                        1 NHLGLVLLVLHYFVEFLFHISRLFYFSDEKYQKGFSLMAVLFVLGRLLTLILSVLTVGFG 60
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
11-DEC-2001 (TrEMBLrel. 19, Last annotation update)
2900019C14RIK PROTEIN (RIKEN CDNA 2900019C14 GENE) (TRH1).
                                                                                                                                334 RR-----SRSRKGTENGVE---NPNRIDSPPKKKEKA 362
                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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67 AVEQGQEREVHGYLSGILDLPAIFFYSVCMIVVHAVVQEYGLDKISKKTHLSKVSTFKFG 126
                                                       120 EAGQLSVFYIVSGIWGMIILASENCLSD----PTLLWKSQP--HNMWTFQMKFFYISQL 172
                                                                                                                              173 AYWFHSFPELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNHLGLLLLMHYAVELLS 232
                                                                              SVCSLLYFGDERYQKGLS-----LWPIVFISGRLVTLIVSVVT--VGLHLAGTNRNGNAL 285
                                                                                                                                                                                                                                245 HIARFAHFVG---RKGLSDPAFKLFNGSFVLVRLGSIIIAVMTFWYGLRQA-ESPFVDIS 300
                                                                                                                                                                                                                                                                                SGNVNVLAAKIAVLSSSCSIQVYITWTLTTVWLQRWLEDANLHVCGRKRRSRSRKGTENG 345
                                                                                                                                                                                                                                                                                                                   301 AGNFNTAVIRINVLLAVILQLFLLYSFVV------FHM-GRFRESNAKKEKKKS 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 348; DB 11; Length 159;
Pred. No. 1.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 AA; 18053 MW; D88C0B3126B0085A CRC64;
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1810049E02RIK PROTEIN (FRAGMENT).
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MGI:1919515; 1810049E02Rik.
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EMBL; AK007839; BAB25296.1;
                                                                                                                                                                                                                                                                                                                                                         346 VENPNRIDSPPKKKEK 361
                                                                                                                                                                                                                                                                                                                                                                                              349 AAAAAAV---PKKEKK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
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Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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09CVJ6;
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RC STRAIN-C57BL/63; TISSUE-HIPPOCAMPUS;
RX MEDLINE-21085660; PubMed-11217851;
RAWANI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kyosawa H., Kondo S., Yamanaka I.,
RA Satto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Saburia M., Batalov S., Casavant T.,
RA Schriml L.M., Staubli F., Sizuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli P., Sizuki R., Tomita M., Wagner L., Washio T.,
RA Brownstein M.J., Bult C., Fletcher C., Fullta M., Gariboldi M.,
R Brownstein M.J., Bult C., Fletcher C., Fullta M., Gariboldi M.,
R Brownstein M.J., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
R Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Basaki H., Sato K., Schogwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schogwald M., Rodriguez I., Sakamoto N.,
RA Sakai H., Sato K., Schogwald K.H., Weitz C., Whittaker C., Willming L.,
RA Hyashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 RRLQLTKGKQNKLNEAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQPHNMMTFQMK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Functional annotation of a full-length mouse cDNA collection.";
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; Pred. No. 1.5e-06;
40; Mismatches 76; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg k.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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EMBL; AK013554; BAB28903.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00389; HOX; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
SEQUENCE 393 AA; 46016 MW; B2038F7A128F816F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K40299.1; -.
2900019C14Rik.
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InterPro; IPR001356; Homeobox.
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EMBL; AY029531; AAK40299.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
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Matches 46; Conservative
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Indels 10;

215 NHLGLLLLMLHYAVELLSSVCSLLYFGDERYQKGLSLWPIVFISGRLVTLIVSVVTVGLH 274

Conservative

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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 ---GKQNKLNEAGQLSVFYIVSGIWGMIILASENCLSDPTLLWKSQ-----PHNMMTFQM 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 KFFYISQLAYWEHS-FPELYFQKVRKQDIPGQLIYIGLHLFHIGGAYLLYLNH-----L 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 ESLPE-----YQDLIFLLFFALFFPVLRFILDRFVFEALAKRMIFGKKTVVNINGR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic and physical analysis of a YAC contig spanning the fungal disease resistance locus Asc of tomato (Lycopersicon esculentum)."; Mol. Gen. Genet. 261:50-57(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brandwagt B.F., Mesbah L.A., Takken F.L.W., Laurent P.L.,
Kneppers T.J.A., Hille J., Nijkamp H.J.J.;
"A longevity assurance gene homolog of tomato mediates resistance t
Alternaria alternata f. sp. lycopersici toxins and fumonisin Bl.";
Proc. Natl. Acad. Sci. U.S. 97:4961-4966(2000).
EMBL; AF198177; AAF67518.1; -.
SEQUENCE 308 AA; 36301 MW; 2BD3378CE53F416D CRC64;
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STRAIN-Y, CN BW SP.
STRAIN-Y, CN BW SP.
STRAIN-Y, CN BW SP.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AX061255; AAL28803.1; -.
                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I; Solanales, Solanaceae, Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Mesbah L.A., Kneppers T.J., Takken F.L., Laurent P., Hille J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.9%; Score 131; DB 10; Length 308; Best Local Similarity 19.5%; Pred. No. 0.00094; Matches 46; Conservative 50; Mismatches 80; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGLPSGSRTLYHYGVKDLATVFFYMLVAIIIHATIQEYVLDKLSRRLQLTK-
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Last annotation update)
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Drosophila melanogaster (Fruit fly).
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SEQUENCE FROM N.A.
STRAIN-CV. VPNT CHERRY;
MEDLINE-20243803; Pubmed-10781105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. VFNT CHERRY;
MEDLINE-99168767; PubMed-10071209;
                                       Lycopersicon esculentum (Tomato).
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                                                                                                                                                                                                    NCBI_TaxID=4081;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nijkamp H.J.;
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ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

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"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                  222 LMLHYAVELLSSVCSLLYFGDERYQKGLS----LWPIVFISGRLVTLIVSVVTVGLH 274
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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; Pred. No. 0.00027;
42; Mismatches 81; Indels 11;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR022151; BAB13972.1;
EMBL; BC009828; AAH09928.1;
InterPro; IPR001356; Homeobox.
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Homo sapiens (Human).
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Best Local Similarity 24.7%
Matches 44; Conservative
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TISSUE=LUNG CARCINOMA;
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**09M6A4** RESULT 14 **Q9M6A4** 

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SQ SEQUENCE 400 AA; 46351 MW; AB586DB2B8111E62 CRC64;
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Search completed: September 6, 2002, 17:20:26 Job time: 635 sec

4.5 Compugen Ltd.

GenCore version Copyright (c) 1993 - 2000

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; Search time 5654.61 Seconds
(without alignments)
8467.413 Million cell updates/sec
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Maximum Match 100%
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 nucleic search, using sw model
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Homo sapiens BAC clone RP11-32609 from 4, complete sequence.
AC093805 AC012532
AC093805.3 GI:18497223
HTG.
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BC018212
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AC022032 A
AC022031 A
AY075393 I
AC014319 I
AC014319 I
AC03726 A
AX192932 S
AC03419 I
AX192932 A
AC010042 A
AX305631 S
AX305631 A
AX305631 A
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Cedroni, M., Abbott, A. and Bielicki, L.
The sequence of Homo sapiens BAC clone RP11-32609
Unpublished (2001)
3 (bases 1 to 165538)
Waterston, R. H.
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Bukaryota, Metazoa, Chordata, Craniata,
Mammalia, Eutheria, Primates, Catarrhini
1 (bases 1 to 165538)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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56.3 1288
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35.1 155623
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19847. .20312
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15850. 15875
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15929. 16234
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5385. .5592
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7152. .742k
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21958. .21983
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20868. .21156
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Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
Submitted (10-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                             Submitted (05-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: chall regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Data from AC013556 was used to finish the clone, AC093805.
Polymorphisms have been identified between AC013556 and AC093805.
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Actual start of this clone is at base position 1 of RP11-32609;
actual end is at base position 165538 of RP11-32609.
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                                                                                                                                                                                                                                                                                                                                                               Center code: WGGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Summarv Stafistice
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: H_NH0326009
Drafting Center: WIBR
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1. .165538
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/db_xref="taxon:9606"
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    .130
    /rpt_family="MalR"

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Waterston, R.H.
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/rpt_family="AT_rich"
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/rpt_family="L2"
28756. .28814
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/rpt_family="Alu"
23503. .23691
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/rpt_family="L2"
25636. .?=?
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26711. .27112
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23715. .23895
                                                                                 /rpt_family="MIR"
24054. .24855
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24966. .25190
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100.0%; Pred. No. 1...
0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1 275 c 276 g 40
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18; Conservative
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I (bases 1 to 1288)
Todo, N., Okuyama, H. Imamura, M., Ishikawa, H. and Nemoto, K. Method of screening of protein
Patent: JP 03075332-T 316 FEB-2001;
SUMITOMO PHARMACEUTICALS CO LTD, NAOKI TODO, HAJIME OKUYAMA, OTOAKI IMAMURA, HIRONORI ISHIKAWA, KIYOMITSU NEMOTO
OS Homo sapiens (human)
Ph 10 03075332-T/3
Ph 17 + MG-2000 JP 2000005488
PR 20-AGG-1999 JP 99P 234764
PI NAOKI TODO, HAJIME OKUYAMA, MOTOAKI IMAMURA, HIRONORI ISHIKAWA, PI KIYOMITSU NEMOTO
PC C12Q1/O2.00133.50, CO7K14/47, A61K38/17, C12N5/10, C12P21/02// PC
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C12Q1/02,G01N33/50,C07K14/47,A61K38/17,C12N5/10,C12P21/02//
(C12P21/02,C12R1:91)
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398 caagcetacgtaacatggaacttaattactctctggcttcagaggtgggtagaagattct 1457	g &	61 CAGAATCATGCGGACATCGTCT
aatattoaggoctcatgtatgaaaaagaaacgtcgagatcttctaaaaaaagaacagaa	Db Qy	121 GAGGGAACAGCAGAAGCATCCA 657 gcagcagaggaacaagccacgg
CCTCATGTATGAAAAGAAAGGGTCGAGATCTTCTAAAAAAAGAACAGAA 1	Db	181 GCAGCAGAGGAACAAGCCACGG
1116 accgagagagagaactccaaacagagcagactgrccgccaaagaggagaga 15// 	oy i	717 gccacggttttcttctacatgc
1578 tottcataatotttgcaagcgcattgattaatgtctgcaaaggaatotgctctttgaggt 1637 	DΒ	241 GCCACGGTTTTCTTCTACATGC 777 gtgttggataaaattaacaaga
ttcttctgcactagagatttttctgtttttgaaaatagttcgtgctcttcggtttttgt	DD QY	301 GTGTTGGATAAATTAAGAGG
izoi Ticritciscaciadadaritticistitisaaaaiasricsissittist 1260 1698 tattaaastottisatottittiaaa 1725	qa	361 GAGTCTGGTCAGTTTAGTGTGT
261 TATTGAACTGTTTCATGTATTTTTAAA 128	Qy	897 atctctgaaaactgcctgtcag
RESULT 3	Qy	957 atgacattcaaatgaagttt
2	QQ	481 ATGACATTTCAAATGAAGTTTT
BD005226 BD005226.1 GI:1863318' JP 03075332-T/1.	QY	1017 cctgaactctacttccagaaaa 
Homo sapiens. Homo sapiens	δ	1077 ggtcttcacctcttccacatt
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	qa	601 GGTCTTCACCTCTTCCACATTA
EEEKENCE I (Dages I to 111U) AUTHORS Todo, N., Okuyama, H., Imamura, M., Ishikawa, H. and Nemoto, K. TTT.R. Method of streening of profession	Qy	1137 cttcttttggtactgcattat
LE MECHOU OI SCIEGHING OI PIONEIN RNAL Patent: JR 93075332-T I 16-FEB-2001; SUMITOMO PHARMACHITICALS CO LTM. NAOKI TODO HALIME OKHVAMA. OTOAKI	qq	661 CTTCTTTGGTACTGCATTATT
IMAMURA, HIRONORI ISHIKAWA, KIYOMITSU NEMOTO COMMENT OS HOMO SADIens (human)	Qy	1197 tttagtgatgaaaagtaccaga
	qq	721 TTTAGTGATGAAAGTACCAG
PF 17-AUG-2000 JP 2000005488 PR 20-AUG-1999 JP 99P 234764	δλ	1257 agacttgtgactttaattgttt
PI NAOKI TODO, HAJIME OKUYAMA, MOTOAKI IMAMURA, HIRONORI ISHIKAWA, PI KIYOMITSI NEMORO	qq	781 AGACTTGTGACTTTAATTGTT
PC C1201/02, G01N33/50, C07K14/47, A61K38/17, C12N5/10, C12P21/02// PC (C12P21/02, C12R1:91)	Qy	1317 aatcggaatcctgatgccctta
CC FH Key Location/Oualifiers	qq	841 AATCGGAATCCTGATGCCCTT
CDS (1). (1107). Location/Qualifiers	Qy	1377 ctgtcgtccagttgcacgatcc
source 11110 /organism="Homo sapiens"	qq	901 CTGTCGTCCAGTTGCACGATC
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Query Match 48.5%; Score 1110; DB 6; Length 1110; Bost Lonal Similarity 100 08. Brod No. 1 20.257.	Oy 4d	1497 tottotaaaaaaagaacagaaa 
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	3 6	
477 atggggctccgtaagaagagcaccaagaacccccgttctcagccaggaattcatcctg 536	7 B	1081 CCGCCAAAGAGGAAAGAGAAAT

tttctacatatcccagttggcttactggtttcatgcttt 1016 wascggagtgggagtggaaacttcaaatagagtagactgt 1556 99acccaactcttatatggaaggctcgtcccatagcatg 956 caagcctacgtaacatggaacttaattactctctggctt :tcctgcgtggggatgttcttcctgctgggggcttgtgttc jttctacttttttttttgtatttggggcacattcatttta TCTTCATAA 1110 tetteataa 1586

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DKINRRMHFSKTKHSKFNESQOLSAFYLESCINGTFILISENSYISDPPILMRAYPHNL
MTFQMKFYTAQLATWFHAFPELYFQKTKKEDIPRQLVYIGLYLFHTAGAYLILLNH
GLVILVYLHYFWEFLFHISRLFYFSDBKYQKGFSLMAVLFVLGRLLTILLSVLTVGFGL
ARAENOKLESSAGNFNYLAVRIAVLAICITOAFMMKFINFQLRRWREHSFFQAPVV
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Submitted (28-JAN-1992) E. Hartmann, Max-Delbrueck-Centr.
Molekulare Med., Robert-Roessle-Strasse 10, 0-1115 Berlin
Location/Qualifiers
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Cai
I (bases I. 0. 2856)
Gorlich, D., Hartmann, E., Prehn, S. and Rapoport, T.A.
A protein of the endoplasmic reticulum involved early
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Pred. No. 1.1e-221;
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/db_xref="SWISS-PROT:001685"
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/organism="canis familiaris"
/db_xref="taxon:9615"
/cell_line="MDCK"
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Nature 357 (6373), 47-52 (1992)
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Matches 1447; Conservative (
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X63678.1 GI:941
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KKKPTYTKGRSSKKGTENGVNGTLTSNVADSPRNKKEKSS"
                     Clone distribution: MGC clone distribution information can be four through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 5 Row: 1 Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657654.
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Contact:

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Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.W.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC000687 2722 bp mRNA linear PRI 12-JUL-2001 Homo sapiens, translocating chain-associating membrane protein, clone MGC:784 IMAGE:3347823, mRNA, complete cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Galthersburg, Maryland;
Web site:
http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                               GTATTAG---CAAGATGGCCTCTTCCAGCAAGGTCATTTTTTAAGTTATCTTTCAGGGT
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Contact: MGC help desk
Emall: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
aaaataaaagtacgaaaaaggtggaagtcaaa----
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Strausberg, R.
Direct Submission
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FNESQQLSAFYLFSCIWGTFILISENYISDPTILWRAYPHNLAFTROMRFYISQLAYW
FHAFPELYFOYTKKEDIPRQLYYIGLYLFHIAGAYLLNLHLGLVLLVLHYFVEFLFH
ISRLFYFSDEKYQKGFSLWAVLFVLGKRLTLILSVLYVGFGLARAENQKLDFSTGNFN
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                                                                                                                                                                                                                                                                                                                   Bos taurus translocation chain-membrane associating protein (tram) mRNA, partial cds.
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I (bases I to 2387)

Clark, T.G., Morris, J., Akamatsu, M., McGraw, R.A. and Ivarie, R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished

2 (bases 1 to 2387)

Clark T.G., Morris, J., Akamatsu, M., McGraw, R.A. and Ivarie, R.D.

Direct Submission

Submitted (06-JAN-1995) Genetics, University of Georgia, Athens, 30602-7223, USA
584
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/organism="Bos taurus"
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Ruzny, D.M., Adams. C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrows, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Babbrows, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Babrows, S.L., Amaratunge, H.C., Are, J.R., Bouck, J., Blagack, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burket, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Chond, T.C., Carcon, T.F., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Douthwaite, K.J., Davas, C., Coyle, M., Edon, C., Coyle, M., Edon, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Ender, D., Esoctto, M., Falls, T., Ferstaquto, D., Edwards, C.C., Ender, J., Esoctto, M., Falls, T., Ferstaquto, D., Edwards, C.C., Ender, J., Edbisi, A., Gao, J., Garcia, A., Garner, T., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Foster, P., Frantz, P., Gabisi, A., Hober, J., Hule, S., Hamilton, K., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, J., Horber, J., Hulyk, S., Hume, J., Jackson, E., Jackson, E., Lid, J., Lu, J., Chordata; Craniata; Vertebrata; Buteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; 1880 cagagataact----goacaattttgcatatcaatgat-actggttcttactcccacca 1933 1760 aaaaaaagattttggttgagactaaattactcatcgtcaaaataatgtcaaaatagtttt 1819 1820 ggggatcaccactatatttttgttttgatttttaacctttcaacattttcctaatgatttg 1879 Eukaryota; Metazoa; Mammalia; Eutheria; Rattus. ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS RESULT AC106086 LOCUS QQ ò a ò q δy qq ŏ

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NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the flnished sequence as soon as it is available and the accession number will be preserved.
                                                 Consensus quality: 127470 bases at least Q40
Consensus quality: 134419 bases at least Q30
Consensus quality: 139475 bases at least Q20
Estimated insert size: 122947; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation
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1 (Dases 1 to 1267)

Todo,N., Okuyama,H., Imamura,M., Ishikawa,H. and Nemoto,K. Paterti of screening of protein
Paterti: JP 03075332-7 4 16-FBB-2001;
SUMITOMO PHARMACEUTICALS CO LTD.NAOKI TODO,HAJIME OKUYAMA, OTOAKI IMAMOTA, HIRONORI ISHIKAWA,KIYOMITSU NEMOTO
OS Homo sapiens (human)
                   1184
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NAOKI TODO, HAJIME OKUYAMA, MOTOAKI IMAMURA, HIRONORI ISHIKAWA,
                                                                                                          1185 ggcctgtttactttagtgatgaaaagtaccagaaaggcatatctctgtgggccattgtg 1244
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/organism="Homo sapiens"
/db_xref="taxon:9606"
1 278 c 275 g 371
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17-AUG-2000 JP 2000005488
20-AUG-1999 JP 99P 23476
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JP 03075332-T/4.
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature gene sets
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 21
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Avalon Pharmaceuticals (US)
Location/Qualifiers
                                                              AX329795
Sequence 304 from Patent WO0194629.
AX329795
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/db_xref="taxon:9606"
278 c 275 q 377
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al Similarity 79.7%;
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Vertebrata; Euteleostomi;

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Hartmann, E.
Birect Submission
Submitted 69-7, Nobert-Roessle-Strasse 10, 0-1115 Berlin
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 1267)
Gorlich,D., Hartmann,E., Prehn,S. and Rapoport,T.A.
A protein of the endoplasmic reticulum involved early
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Pred. No. 1e-168;
0; Mismatches 216;
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/db_xref="taxon:9606"
/cell_line="Hela"
                                                                                                                                                                         H.sapiens mRNA for TRAMP protein.
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Nature 357 (6373), 47-52 (1992)
92244357
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/gene="TRAM"
/codon_start=1
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traM gene; TraM protein.
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122. .1246
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Best Local Similarity 79.7%;
Matches 907; Conservative (
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                                               15;
                 Length 1267;
                                               Indels
             Score 742.4; DB 6;
Pred. No. 1e-168;
0; Mismatches 216;
             32.4%;
llarity 79.7%;
Conservative
                              Similarity
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Best Local S:
Matches 907,
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                                           1 (bases 1 to 2720)

Hartmann, E.

Direct Submission
Submitted (09-APR-2001) Biologie, Universitaet Lu Allee 160, Luebeck 23538, Germany
Location/Qualifiers

1 . 2720

//Organism="Mus musculus"
//db_xref="taxon:10090"
//clone="RZPD clone IMAG9998K219524q2"
36 . 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.0%; Score 733; DB 10; 74.0%; Pred. No. 2.3e-166; live 0; Mismatches 330;
                    Chordata;
                                       Rodentia;
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Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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KGAIIEVALQYNVTRPATEEQATESASLYHYGIKDLATVLFYMLVAIIIHAIIQEYVL
MTRINHRHFSKTKHSKFNESQOLSAFYLFACWGFFILISRBYISDPTILMRAYPHNL
MTRQTKFFT1SQLAYMLHAFPELYFQKTKKEDIPRQLVYIGLYLFHIAGAYLLNLHHL
GLVLLVLHYPFEFLFHISRLFFSDBKYQKGFSLMAVLFVLGRLTTILSVLTYGFGL
ARAENOKLDFSTGNFNVLAVRIAVLASICITQAFMMKFINFQLRRMREHSAFQAPPV
KRKPAVTKGRSSRKGTENGVNGTVTSNGADSPRNRKEKSS"
                                                                                                                                                                                                                                                    be found
                                                                                                                                                                              Garcia,
                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/Lini. at: http://image.llnl.gov Series: IRAK Plate: 17 Row: j Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
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/db_xref="taxon:10090"
/clone="MGC:11724 IMAGE:3967323"
/tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy."
/clone_lib="MCI_GGAP_Mam1"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon.D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Gar.
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.
Muzny, D.M., Glbbs, R.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2819)
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Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
Homo sapiens chromosome 4 clone RP11-724E21 map 4, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads * and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for * identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. * However, it should not be assumed that this clone * will be sequenced to completion. In the event that the record is updated, the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 4, clone RP11-724E21
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Center clone name: 724_E_21
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Mammalia; Eutheria; Primates;
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NAOKI TODO, HAJIME OKUYAWA, MOTOAKI IMAMURA, HIRONORI ISHIKAWA,
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S Todo, N., Okuyama, H., Imamura, M., Ishikawa, H. and Nemoto, K.
Method of screening of protein
L Patent: JP 03075332-T 2 16-FEB-2001;
SUMITOMO PHARMACEUTICALS CO LTD, NAOKI TODO, HAJIME OKUYAMA, OTOO
IMAMURA, HIRONORI ISHIKAWA, KIYOMITSU NEMOTO
OS Rattus Sp. (rat)
PD 16-FEB-2001
PP 17-AUG-2000 JP 99P 234.764
PR 20-AUG-1999 JP 99P 234.764
PI NAOKI TODO, HAJIME OKUYAMA, MOTOAKI IMAMURA, HIRONORI ISHIKAW
PI KIYOMITSU NEMOTO
PC C1201/02.G01N33/50.C07K14/47, A61K38/17, C12N5/10, C12P211/02.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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268 c 288 g 2
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RASTORAKGRASKGNGNYTVYSNGADSPRSRKEKHS"
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                    Direct Submission
Submitted (10-APR-2001) Biologie, University Lubeck, Ratzeburger
Allee 160, Lubeck 23538, Germany
Location/Qualifiers
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Pred. No. 3.3e-112;
0; Mismatches 347;
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16. .1137
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Hartmann, E.
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proliferation for use in treatment and diagnosis of cancer including sarcomas of high malignancy \,
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This sequence represents the DNA encoding an endoplasmic reticulum protein (WAR-1). The invention includes rat and human WAR-1 sequences, expression vectors containing the DNA, cells transformed with the expression vector, antibodies against WAR-1, and probes and primers which hybridise to the DNA encoding WAR-1. The WAR-1 protein inhibits the proliferation of cancer cells, and is used in the treatment and diagnosis of cancers including highly malignant sarcomas. ö ctattgttgttgttataattaatgatctgaagaataaccagagctctataggtttatcatgat 120 300 Gaps tatagggcacgcgtggtcgacggcccgggctggtactgggattttgctgttattattatg 60 gagcagccagggggaggcagctgcggctcgccggtgagtatccgggaagcgccaccatgg 480 ggctccgtaagaagagcaccaagaaccccccgttctcagccaggaattcatcctgcaga 540 9 600 099 099 tggataaaattaacaagagaatgcagttcaccaaagcgaaacaaaacaagtttaacgagt 840 taggggcgcggctcgatttccttccctgcctccgccgtcccctggtgcgcatgctca gaacagcagaagcatccatcgtgtttctcactcttcagcacagtgttgctgtccctgcag DB 21; Length 2288; ö Indels Sequence 2288 BP; 612 A; 467 C; 503 G; 706 T; 0 other; ; 0 Ouery Match 100.0%; Score 2288; Best Local Similarity 100.0%; Pred. No. 0; Matches 2288; Conservative 0; Mismatches Claim 2; Fig 1; 89pp; Japanese. 241 61 61 121 121 181 181 241 301 301 361 361 421 421 481 601 601 199 661 781 721 ò a ò g ОВ ò à qq δ qq δy οp δý Q ŏ g QQ δ Qγ g φ a ò qq δ 셤 ò

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                                                                                    The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo and gene mapping, and in recombinant production of (II). The
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polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human changes of the invention.

Coliagnostic coding sequences of the invention appear in the printed specification, but was obtained in electronic format directly from WIPO
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been stolated and nuclocities sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length easily human of the construction of the full length cDNA easily human of the construction of the full length cDNA easily human of the construction of the full length cDNA easily human of the construction of the full length cDNA easily human of the construction of the full length cDNA easily human of the construction of the full length easily human of the construction of the full length cDNA easily human of the construction of the full length easily human of the construction of the full length easily human of the construction of the full length easily human of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction 
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11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
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474 accatggggctccgtaagaagacaccaagaaccccccgttctcagccaggaattcatc  181 accatggggctccgtaagaagacaccaagaaccccccgttctcagccaggaattcatc  182 ctgcagaatcatgcggacatcgtctctgcgtggggatgttcttcctgctggggcttgtg  183 ttgcagaatcatgcggacatcgtctctctgcgtggggatgttcttcctgctgggggcttgtg  184 ttgggggaacagcagaagcatccatgtgtttctcactcttcagcaaggttgctgtg  185 ttcgagggaacagcagaagcatccatgtgtttctcactcttcagcaaggttgtgtgtg	atcccagttggcttactggtttc atcccagttggcttactggtttc acccagttggcttactggtttc acaagacatccctcgtcaacttg 	Oy 1194 tactttagtgatgaaaagtaccagaaaggcatatctctgtgggccattgtgttatcttg 1253   11111111111111111111111111111111111	Oy 1434 cttcagaggtgggtagaagattctaatattcaggcctcatgtatgaaaagaaacggtcg 1493

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and the recombination process used to produce the polypeptide. The present invention also discloses the method of applying the polypeptide and polynucleotides in treating immunological disorder, malignant tumour cancer and other diseases. The antagonist resisting the polypeptide and its treatment effect is also disclosed. Diagnosis and determination method based on the discrimination of the mutation in the nucleic acid sequence and the change in the polypeptide expression level, and the application of the polynucleotides encoding the BioTRAM. The present sequence represents the coding sequence of the novel human BioTRAM protein as described in the invention.
   protein (BioTRAM), polynucleotides encoding this polypeptide
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Sequence 1517 BP; 459 A; 262 C; 308 G; 488 T; 0 other;

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cell membrane protein; cytostatic; CNS active; antiallergic;
antirheumatic; nervous system disorder; immune disorder; alle
rheumatism; skeletal disorder; ss.
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The present invention describes a screening method for secretory and membrane proteins consisting of transformation of a cell with separate expression vectors for the sense and antisense RNA of DNA encoding an endoplasmic reticulum membrane protein participating in endoplasmic reticulum transport of proteins. Also described are: (1) secretory and cell membrane proteins identified by the screening method; (2) drug compositions containing these proteins; (3) host cells transformed by the separate expression vectors of the method; and (4) the preparation of secretory and cell membrane proteins by culture of the transformants. The method can be used for the identification and preparation of proteins for use in the treatment and prevention of diseases such as cancer, disorders of the nervous system, immune disorders (including allergies and rheumatism) and skeletal disorders. The present sequence
                                                                                         Transformation of a cell with separate vectors expressing the sense antisense strands of WAR-1 DNA for screening secretory and membrane \,
                                                                                                                                                                                            Example 1; Page 68-71; 79pp; Japanese
                                                                                                                                                proteins expressed by the cell
                      WPI; 2001-202940/20.
P-PSDB; AAB70695.
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Sequence 1288 BP; 331 A; 275 C; 276 G; 406 T; 0 other;

ő 480 300 360 420 677 737 797 857 917 gacccaactcttatatggaaggctcgtccccatagcatgatgacatttcaaatgaagttt 977 Gaps 181 atcgtgtttctcactcttcagcacagtgttgctgtccctgcagcagaggaacaagccacg ggctcaaagtccctctattattgtgtgtcaaagatttggccacggttttcttctacatg agaatgcagttcaccaaagcgaaacaaaacaagtttaacgagtctggtcagtttagtgt ttctactttttttttttgtatttggggcacattcattttaatctctgaaaactgcctgtca ö Length 1288; Indels 22; ; 0 B 56.3%; Scc. 100.0%; Pred. No. v. 0, Mismatches Best Local Similarity 100. Matches 1288; Conservative Query Match 438 421 819 738 798 361 828 978 541 618 301 918 481 à g ö 셤 δ g ò q δy g 8 ó 셤 ò g ò g ò

WO200114582-A1

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661 actggagcttatctcttgtacttgaatcatttgggacttcttcttttggtactgcattat
                                                                                                  aacggagtgggagtggaaacttcaaatagagtagactgtccgccaaagaggaaagagaaa
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                                            actggagcttatctcttgtacttgaatcatttggacttcttcttttggtactgcattat
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The present invention describes a screening method for secretory and membrane proteins consisting of transformation of a cell with separate expression vectors for the sense and antisense RNA of DNA encoding an endoplasmic reticulum membrane protein participating in endoplasmic reticulum membrane proteins. Also described are: (1) secretory and cell membrane proteins identified by the screening method; (2) drug compositions containing these proteins; (3) host cells transformed by the separate expression vectors of the method; and (4) the preparation of secretory and cell membrane proteins by culture of the transformants. The method can be used for the identification and preparation of proteins for use in the treatment and prevention of diseases such as cancer, disorders of the mervous system, immune disorders (including allergies and rheumatism) and skeletal disorders. The present sequence
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100.0%; Pred. No. 6.4e-282;
Live 0; Mismatches 0;
                                                                                                                                                     Ishikawa H,
                                                                                                                                                                                                                                                                                                      Claim 2; Page 62-65; 79pp; Japanese.
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                                                                                                                                                       Imamura
                                                                                                                                                                                                                                                                       proteins expressed by the cell
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                                                  17-AUG-2000; 2000WO-JP05488
                                                                                   99JP-0234764
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Matches 1110; Conservative
                                                                                                                                                     Tohdoh N, Okuyama H,
                                                                                                                                                                                     WPI; 2001-202940/20.
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                                                                                   20-AUG-1999;
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diagnosis; cytostatic; poliferative; vulnerary; immunomodulator; antidabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antidifammatory; antithyroid; antilheratic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coaquiant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; haematopoletic cell disorder; autoimmune disorder; haematopoletic caldiamation; immune disorder; antipsoriatic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
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                                                                                                                                                                                                                                         Human; cancer associated gene; cancer antigen; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cancer associated gene sequence SEQ ID NO:204
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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB4398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antisthmatic; antitherary; immunomodulator; antidiabetic; antisthmatic; antitherary; immunomodulator; antidiabetic; antisthmatic; antitherary; immunomodulator; coagulator; antidiamatory; antipsortatic and antiangiogenic. The correction includes and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Complyuciectides, polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Complyuciectides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune cells, to treat disorders of the presses and organ crejection, modulate haemostatic or thrombolytic activity, modulate celection, modulate haemostatic or thrombolytic activity, modulate capacitis and antagonists may be also be used in drug screens. AAC7849, the pressent and antagonists may be also be used in the exemplification of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the conte
                                                                                                                                                                                                                                                                                                                                                                           isolated nucleic acids comprising sequences encoding for treating or diagnosing e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 776-777; 2352pp; English
                                2000WO-US05882
                                                                                          99US-0124270
                                                                                                                                                        SCI
                                                                                                                                                        (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                  Ruben SM;
                                                                                                                                                                                                                                                                             WPI; 2000-587533/55.
P-PSDB; AAB43601.
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                                                                                          12-MAR-1999;
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Sequence 2833 BP; 888 A; 504 C; 506 G; 931 T; 4 other;

16; 265 385 584 644 325 704 764 445 884 565 524 Gaps ggaagcgccaccatggggctccgtaagaagagcaccaagaacccccccgttctcagccag gaattcatcctgcagaatcatgcggacatcgtctcctgcgtgggatgttcttcctgctg gggcttgtgttcgagggaacagcagaagcatccatcgtgtttctcactcttcagcacagt gttgctgtcctgcagcagaggaacaagccacgggctcaaagtccctctattattggt 41.0%; Score 937.6; DB 21; Length 2833; 75.5%; Pred. No. 2.7e-236; 63; Indels 0; Mismatches 389; Conservative Similarity Query Match Best Local Simil Matches 1394; ( 146 206 386 465 525 266 645 326 705 765 585 825 g δ g g ò g g õ g ò à ò ò

ataactgc----acaattttgcatatcaatgatactggttcttactcccaccagtgttt 1939 | ||||| aaaactatttacaaaaattccacatatcagtgatacaatttcttgctgtcaccaatttt 1629 ggcctgttttactttagtgatgaaagtaccagaaaggcatatctctgtgggccattgtg 1244 aaaattgctgttctgtcgtccagttgcacgatccaagcctacgtaacatggaacttaatt 1424 1226 acattaacttcaaatgtagcagactctccccggaataaaaaaagagaaatcttcataatga 1285 ctagagatttttctgtttttgaaaat--agttcgtgctcttcggtttttgttattgaact 1706 gtttcatgtatttttt--aaagacatttgaggggaggaggattattatgaatgggaaaaa 1764 catttgggacttcttcttttggtactgcattattttgttgaattactttcccacatgtgc 1184 tttatcttgggtagacttgtgactttaattgtttccgtactcactgttgggtttcacctg 1304 gctggatcgcagaatcggaatcctgatgcccttactggaaatgtaaatgtgttggcagct 1364 gtggaaacttcaaatagagtagactgtccgccaaagaggaaagagaaatcttcataat-c aatattttagcttagactaagctacctgccttcaaaata------gtttaggga acattcattttaatctctqaaaactgcctgtcaqacccaactcttatatggaaggctcgt actetetggetteagaggtgggtagaagattetaatatteaggeeteatgtatgaaaag aattttcagcttcgaaggtggaagggaacattctgcttttcaggcaccagctgtgaagaag aagattttggttgagactaaattactcatcgtcaaaataatgtcaaaatagttttgggga ccccatagcatgatgacatttcaaatgaagtttttctacatatcccagttggcttactgg tcaccactatatttttgtttttgatttttaacctttcaacattttcctaatgatttgcagag aaacggtcg------agatcttctaaaaaaagaacagaaacggagtg 1570 1005 1245 1046 1425 1106 1286 1649 1406 1825 1065 1125 998 1305 1365 1346 1707 1765 1464 1512 945 989 746 926 g ŏ g οy g ò g ò 원 ò g ò g ò g ò 셤 à q ογ g ò 8 δ 8 οy 8 ò Q ò 용 οχ g ŏ g

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Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; gene therapy; antimicrobial; hepatotropic; immunosuppressive; antirheumatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production, and the cell is also useful for identifying compounds that modulate expression of the polynucleotide sequences encoding the secreted proteins. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
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and Crohn's disease
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sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis). The polynucleotide sequences of the invention are also useful in gene therapy. As562214.AAS62818 represent the cDNA sequences of the
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                                                  that encode for novel human secreted proteins
                                                                          825 A; 498 C; 505 G; 928 T; 0 other;
                                                                                                             Score 923.4; DB 24;
Pred. No. 1.5e-232;
0; Mismatches 391;
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llarity 75.4%;
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cancer cell proliferation inhibitor;

nucleotide sequence

norvegicus.

99WO-JP05631

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diagnosis; cancer; sarcoma; rat; ds
          Endoplasmic reticulum; WAR-1;
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This sequence represents the DNA encoding an endoplasmic reticulum protein (WAR-1). The invention includes rat and human WAR-1 sequences, expression vectors containing the DNA, cells transformed with the expression vector, antibodies against WAR-1, and probes and primers which hybridise to the DNA encoding WAR-1. The WAR-1 protein inhibits the proliferation of cancer cells, and is used in the treatment and diagnosis of cancers including highly malignant sarcomas.
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Pred. No. 1.1e-200;
0; Mismatches 563;
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P-PSDB; AAY98146.
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13-OCT-1998;
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02-MAY-2000;
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2141 2081 ttottoagaacgggtcgtgcttttgaatattgctaatgtattgtctaatgtgttttt-- 1691 synthesizing full length cDNA clones and their Η; aagacatttgaggggaggaggattattatgaatgggaaaaaaagattttggttgagacta tatcaatgatactggttcttactcccaccagtgtttcataatactaacaagatggtctct gcaaagtggtttgttttctcaatgttctcctgcaggataaagtggaaaatctgataaagg tagtgetteateeceatttaaaaaaacacagtactaatgggtaacacatatggaggtttg ------aaggttttgcagacgtatgagtggggggttgagggcta aaccactcagcctctaaatacagtcagaatagttaacgg----accaacatcttatttag tgatttttaacctttcaacatttttcctaatgatttgcagagataactgcacaattttgca cataaataatagt----ttcctgcttccaatgttctttatcgaattaacaagtctgcta cctagcaagattatgtgtttaatgcttgctttggggtaaaat--aaaagtacgaaaaag Kawai Y; T, Koga SS. Human; full length cDNA; cDNA synthesis; oligo-capping; Ishii S, S, Otsuki Hayashi K, K, Kojima NO: 134 Human cDNA 5'-end sequence, SEQ ID Isogai T, 1 T, Nagai ВР 802 99JP-0194486. 2000JP-0118774. 2000JP-0183765. 07-JUL-2000; 2000EP-0114089 entry) CDNA; Nishikawa T, I su A, Sugiyama Primers useful for (HELI-) HELIX RES INST

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                    The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the CDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA assily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atgatgacatttcaaatgaagttttctacatatccc-agttggcttactggtttcatgc 1012
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SEQ ID NO 134; 1380pp + sequence listing; English.
                                                                                                                                                                                                                                                                    12; Indels
                                                                                                                                                                                                Sequence 802 BP; 186 A; 200 C; 193 G; 220 T; 3 other;
                                                                                                                                                                                                                                          Score 761.6; DB 22
Pred. No. 3.1e-190;
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98.3%;
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Claim 2;
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in
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Note: The sequence data for this patent did not form part of the pr
specification, but was obtained in CD-ROM format directly from EPO.
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. T, Koga
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                                                                                                                                                                                                                                                                                                                                                                       SS.
                                                                                                                                                                                                                                                                                                                   Human cDNA clone representative sequence, SEQ ID NO: 2297
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Pred. No. 3.1e-190;
0; Mismatches 12;
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11-JAN-2000;
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                                                             high level in normal prostatic tissue and
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                                                         New nucleic acid expressed at high level in normal prostatic tissue are encoded polypeptides, used to treat cancer and screen for therapeutic
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Pred. No. 1.8e-168;
0; Mismatches 213;
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Best Local Similarity 79.1%;
Matches 888; Conservative
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1999-519629/44
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                                                               gtaacatggaacttaattactctctggcttcagaggtgggtagaagattctaatattcag
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The present invention describes a screening method for secretory and membrane proteins consisting of transformation of a cell with separate expression vectors for the sense and antisense RNA of DNA encoding an endoplasmic reticulum membrane protein participating in endoplasmic reticulum transport of proteins. Also described are: (1) secretory and cell membrane proteins identified by the screening method; (2) drug compositions containing these proteins; (3) host cells transformed by the separate expression vectors of the method; and (4) the preparation of secretory and cell membrane proteins by culture of the transformants. The method can be used for the identification and preparation of proteins for use in the treatment and prevention of diseases such as cancer, disorders of the nervous system, immune disorders (including allergies and rheumatism) and skeletal disorders. The present
     and
Transformation of a cell with separate vectors expressing the sense antisense strands of WAR-1 DNA for screening secretory and membrane
                                                                                                         Claim 3; Page 65-68; 79pp; Japanese.
                                                       proteins expressed by the cell
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Sequence 1092 BP; 260 A; 268 C; 288 G; 276 T; 0 other;

atgacatttcaaatgaagtttttctacatatcccagttggcttactggtttcatgctttt 1016 1017 cctgaactctacttccagaaaaccaaaaacaagacatccctcgtcaacttgtctacatt 1076 536 596 716 237 776 297 836 357 896 417 926 477 537 Gaps 9 atggggctccgtaagaagagcaccaagaaccccccgttctcagccaggaattcatcctg cagaatcatgcggacatcgtctcctgcgtggggatgttcttcctgctgggggcttgtgttc gccacggttttcttctacatgctggtggcaatcattattcatgccacaattcaggaatat gecacagtgttcttctacatgctggtggccatcatcattcacgccaccattcaggagtac ggtcttcacctcttccacattactggagcttatctcttgtacttgaatcatttgggactt gagggaacagcagaagcatccatcgtgtttctcactcttcagcacagtgttgctgtccct gtgttggataaaattaacaagagaatgcagttcaccaaagcgaaacaaaacaagtttaac atctctgaaaactgcctgtcagacccaactcttatatggaaggctcgtcccatagcatg Length 1092; 18; Indels Score 647.8; DB 22; Pred. No. 3.4e-160; 0; Mismatches 247; Query Match 28.3%; Best Local Similarity 76.1%; Matches 844; Conservative 0 477 897 1077 537 61 597 121 657 179 717 238 177 298 837 358 957 d g g qq g Db ŏ ò ·δ δ ò ö ò g ò g ð g

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T, Koga
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S, Otsuki
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K, Kojima
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T, Nagai
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11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
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ID AAK92492 standard; cDNA;
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su A, Sugiyama
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cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA asily without any special methods. The present sequence is the nucleotide sequence of the 3'-end of a cDNA provided in the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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                                                                                                                                                                                                                                   Length 545;
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                                                                                                                                                                          Sequence 545 BP; 185 A; 108 C; 81 G; 170 T; 1 other
                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                       .4e-122;
es 17;
                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                 Score 504.4; E
Pred. No. 1.4e-
0; Mismatches
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                                                                                                                                                                                                                                 22.0%;
96.8%;
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                                                                                                                                                                                                                                                     Best Local Similarity 96.8
Matches 514; Conservative
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nucleic acids that encode them, including immunogenic fragments of the proteins. Also included are expression vectors expressing the proteins. Also included are expression vectors expressing the proteins and antipon protein and antipon protein. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate breast tumour protein expression, i.e. breast tumours and breast cancer e.g by gene therapy. The nucleic acids and their complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The proteins, nucleic acids and antibodies may be used in assays to defentify modulators (e.g. antagonists) of breast tumour protein contents for detecting the presence of the proteins in expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down regulate the prevence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immuno purification diagnostic techniques. The present sequence is much which is a presst tumour protein and activity and in other immuno purification diagnostic techniques. The present sequence is
                                                                                                                                                                                                       Hepler WT;
                                                                                                                                                                                                                                                                                                    Breast Tumour Proteins and nucleic acids useful for the prevention, diagnosis and treatment of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to isolated breast tumour proteins and
                                                                                                                                                                                                       Harlocker SL,
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                                                                                                                                                                                                       Xu J,
                                                                                                                                                                                                                                                                                                                                                                              Claim 37; Page 266; 297pp; English.
                                                                                                                                                                                                    Mitcham JL,
                       2000US-0551621.
2000US-0590751.
2000US-0604287.
2000US-062405.
                                                                                                                                                                                                  Dillon DC,
                                                                                                                                                  (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                    WPI; 2001-611721/70
                       17-APR-2000;
08-JUN-2000;
22-JUN-2000;
20-JUL-2000;
                                                                                                                                                                                                    Jiang Y,
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641 cagigitigotigiccotigoagoagaagaacaagocacgggotcaaagiccotctatiatta 700 642 CAATGTCACCCTCCCAGCAACAGAACAAGCTACTGAATCAGTGTCCCTTTATTACTA 583 Gaps ö Length 642; Query Match 21.3%; Score 486.8; DB 22; Length Best Local Similarity 84.9%; Pred. No. 6.4e-118; Matches 545; Conservative 0; Mismatches 97; Indels g ò

ö 1001 ctggtttcatgcttttcctgaactctacttccagaaaaccaaaaaacaagacatccctcg 1060 941 tcgtccccatagcatgatgacatttcaaatgaagtttttctacatatcccagttggctta 1000 701 tggtgtcaaagatttggccacggttttcttctacatgctggtggcaatcattattcatgc 760 880 881 gggcacattcattttaatctctgaaaactgcctgtcagacccaactcttatatggaaggc 940 ò 셤 δ 셤 ò 셤 ద ò 셤 ò

222 TCAGCTTGTCTACATTGGTCTTAACCTCTTCCACATTGCTGGAGCTTACCTTTTGAACTT gaatcatttgggacttcttcttttggtactgcattattttgttgaattactttcccacat 162 GAATCATCTAGGACTTGTTCTTCTGGGGCTACATTATTTTGTTGAATTTCTTTTCCACAT 1241 tgtgtttatcttgggtagacttgtgactttaattgtttccgt 1282 TCTTTTTGTTTTGGGAAGACTTCTGACTTTAATTCTTTCAGT 1121 42 g ŏ 쉽 ò g ö

Search completed: September 6, 2002, 14:57:42 Job time: 9876 sec

Sequence 19, Sequence 15, Sequence

Sequence

Sequence Sequence

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Title: Perfect :

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APPLICATION NUMBER: US/08/232,463
        US-08-617-860B-19
US-09-007-119-15
US-08-929-416-287
US-08-928-416-287
US-08-928-416-191
US-08-998-416-191
US-08-998-416-191
US-08-998-416-683
US-08-998-416-534
US-08-998-416-534
US-08-998-416-534
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US-08-998-416-534
US-08-98-416-287
US-09-182-816-22
US-09-182-816-22
US-09-182-816-22
US-09-182-816-22
US-09-471-528-24
                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F.
CORRESPONDENCE SOURCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APFLICATION
TILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
TELEPHONE: (703)883-4109
                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suite
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
CITY: Alexandria
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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ZIP: 22313-0299
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CITY:
STATE:
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(without alignments)
5788.541 Million cell updates/sec
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Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 172, App
Sequence 100, App
Sequence 1, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 28, Appli
Sequence 6, Appli
Sequence 6, Appli
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1, Appli
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
            version 4.5
- 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-316-083-2

US-09-316-083-2

US-09-004-838-93

US-08-954-441-1

US-09-9134-681C-6

US-09-91-906-3

US-08-68-91

US-08-954-16-472

US-08-956-3

US-08-98-416-472

US-09-561-825-1

US-09-561-825-26

US-09-561-825-26

US-09-561-825-26

US-09-561-825-26

US-09-61-825-26

US-08-444-083-6

US-08-443-130-6

US-08-443-130-6

US-08-443-130-6

US-08-848-911-6

US-08-898-911-6
                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-377-648-4
US-08-487-826B-13
US-09-561-825-29
                                                                                                                                                                                                                                383533 segs, 122816752 residues
                                                                                    6, 2002, 15:16:46
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                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                             nucleic search, using sw model
                                                                                                                                                                                         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
            GenCore (c) 1993
                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                         US-09-807-470-3
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Match Length
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19124
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                                                                                                                                                      score:
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40.8
339.8
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5150 AGAATTTTCTTGATCATTAGTTAATTTTAGTTGCCTTTWTATTTTTAATGTTGT-CTT 5092
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14.1%; Pred. No. 0.49;
                                                                                                                                                                                                   APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches 264; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                              3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAMBER ELINDORN, GREGGORY P.
REGISTRATION NUMBER: 38,440
REGISTRATION NUMBER: 38,440
REFERONCE/DOCKET NUMBER: 023070-078810US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEO ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 5506 base pairs
TYPE: nucledc acid
STRANDEDNESS: single
    2218 atcaaaatatcattaattaatataaaaa 2245
                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "RG2D"
                                                                                                     RESULT 3
1S-09-004-818-93/C
'Sequence 93, Application US/09004838
'Patent No. 6350933
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-300-4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
nounter: IBM PC compatible
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Best Local Similarity 44.15
Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 1..5506
; OTHER INFORMATION:
US-09-004-838-93
                                                                                                                                                                                                                                                                                                                                                                                                           California
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                                                                                                                                                                                     GENERAL INFORMATION:
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MOLECULE TYPE:
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  DB 1; Length 7218;
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Pred. No. 0.044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: The Institute of Physical and Chemical Research
TITLE OF INVENTION: Endonuclease
FILE REFERENCE: PH-651
CURRENT APPLICATION NUMBER: US/09/316,083A
CURRENT FILING DATE: 1999-05-20
EARLIER APPLICATION NUMBER: J998/141861
EARLIER APPLICATION NUMBER: J988-05-22
NUMBER OF SEQ. ID NOS: 38
SOFTWARE: PATENTIN VET. 2.0
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1209 aagtaccagaaaggcatatctctgtgggccattgtgtttat 1249
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                     1 Similarity 5.2%; Pred. No. 1.7e-05; 21; Conservative 221; Mismatches 159;
Score 58.2; DB 1 Pred. No. 1.7e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.9%;
  2.5%;
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Matches 112, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)..(1428)
US-09-316-083-2
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LENGTH: 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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Query Match
                         Best Local
                                       Matches
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APPLICANT: Williamson, Kim C.
APPLICANT: Kaslow, David C.
TITLE OF INVENTION: Cloning and Expression of Plasmodium
TITLE OF INVENTION: faliciparum Transmission-Blocking Target Antigen, Pfs230
                           1856 tttcaacattttcctaatgatttgcagagataactgcacaattttgcatatcaatgatac 1915
                                                                                     1916 tggttcttactcccaccagtgtttcataatactaacaagatggtctctcctagcaagatt 1975
                                                                                                              1976 atgtgtttaatgcttgctttggggtaaaataaaagtacg-aaaaaggtggaagtcaaatc
                                                                                                                                                                                                    2035 agtattctgtaattgttagaatttattttttaagaacttacaactcagaaaagattgcta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPOURE: IBM PC compatible
COMPOURE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,441
FILING DATE: 20-OCT-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,170
FILING DATE: 13-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/010,409
FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENE/COCKET NUMBER: 015280-113110US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9615 base pairs
                                                                                                                                                                                                                                                                                                                                                  2095 gactcaccaaaataataatgttctttatttt 2126
                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08954441 Patent No. 6316000 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two Embarcade
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149..9556
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; LOCATION:
US-08-954-441-1
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Patent No. 573372
GENERAL INFORMATION:
APPLICANT: Williamson, Kim C.
APPLICANT: Waslow, David C.
TITLE OF INVENTION: Cloning and Expression of Plasmodium
TITLE OF INVENTION: faliciparum Transmission-Blocking Target Antigen, Pfs230
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
2112 aatgttctttattttacaggtagtgattattagtgcttcatccccatttaaaaaaacaca 2171
                                                                                                                                                                                                                                          2052 agaatttatttttaagaacttacaactcagaaaagattgctagactcaccaaaataata 2111
                                                                                                                                                                                                4851 AACTGGTGTGACAATGAGTTAAGTGAGATTGACTAGTTTCCACTTCTACCATCTTAAAAA 4792
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                                                                                                                                                                                                                                                                                                                            2232 aattaatataaaaatattaaaatcattcctgtccattccacttgtaaatgggaatt 2287
                                                                                                                                                                                                                                                                                                                                                       Length 9636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 40.8; DB 1; Length 9 49.3%; Pred. No. 0.83; tive 0; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/323,170B FILING DATE: 13-OCT-1994 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/010,409 FILING DATE: 29-JAN-1993 ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Quine, Jonathan A.

REGISTRATION NUMBER: P-41,261

REFERENCE/DOCKET NUMBER: 015280-113100US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEPHONE: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 9636 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 49.3
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       San Francisco
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149..9556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
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US-08-323-170B-1
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US-08-323-170B-1
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TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
TITLE OF INVENTION Hypohydrotic ectodermal dysplasia genes and proteins
CURRENT APPLICATION NUMBER: US/09/342,681C
CURRENT FILING DATE: 1999-06-29
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 123
SOUTHARE: Patentin Ver. 2.1
                                                                                                           3000 TIGATACATTTACCTTAAAATGTAATGATAAAAACACAATATCCAAATATCGAGATAT 3059
                                                                                                                                                                    1916 tggttcttactcccaccagtgtttcataatactaacaagatggtctctcctagcaagatt 1975
                                                                                                                                                                                                           3060 TTCCTAAAACATTAAAAGATAAAAGGAAGTATTAAAATTTAGATCTTGATATACAATATC 3119
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                                                                                                                                                                                                                                                      atgititiaaigcitigcititggggiaaaataaaagtacg-aaaaaggiggaagtcaaaic 2034
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    Length 9636;
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Score 40.8; DB 4;
Pred. No. 0.83;
); Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                      2095 gactcaccaaaataataatgttctttatttt 2126
                                                                                                                                                                                                                                                                                                                                                                                                                                             3240 CATATAAAAATCATAAAGATGTGAAATATTT 3271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-342-681C-6; Sequence 6, Application US/09342681C; Patent No. 6355782
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1.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 47.1
Matches 122; Conservative
                                         Conservative
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US-09-342-681C-6
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                      Matches 134;
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Query Match
Best Local
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APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: CL001151CIP CURRENT APPLICATION NUMBER: US/09/797,906 CURRENT PILING DATE: 2001-03-05 SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sim, Kim L.
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Neer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1684 tetteggtttttgttattgaactgttteatgtatttttaaagaeatttgaggggaggag 1743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1804 atgtcaaaatagttttggggatcaccactatattttgttttgattttaacctttcaac 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: 620 Newport Center Drive 16th Floor
Newport Beach
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39.8; DE Pred. No. 4.6; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; Sequence 3, Application US/09797906
; Patent No. 6329188
                                                                                                                                                                                                                                                                                                                                                                            , LUCATION: (1)...(84495); OTHER INFORMATION: n = A,T,C OF US-09-797-906-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92; Conservative
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)...(84495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                              SEQ ID NO 3
LENGTH: 84495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-487-826B-13
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Gaps
      TITLE OF INVENTION: Methods and Compositions for Immunomodulation FILE REFERENCE: 9579-21
CURRENT APPLICATION NUMBER: US/09/570,367C
CURRENT FILING DATE: 2000-05-05
PRIOR PLILING DATE: 1997-11-07
NUMBER OF SEQ 1D NOS: 22
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(308..370, 1136..1261, 6369..6428, 7198..7353)
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                                                                                                                                                                                                                                                                                                                           Length 2791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Fabijanski, Steven F.
APPLICANT: Arnison, Paul G.
TITLE OF INVENTION: BINARY CRYPTOCYTOTOXIC METHOD OF HYBRID
TITLE OF INVENTION: SEED PRODUCTION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PCF Compatible
COMPUTER: IBM PCF Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,096
FILING DATE: 22-MR-1993
CLASSIFICATION BATA:
APPLICATION NUMBER: US 07/556,917
FILING DATE: 20-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA91/00255
FILING DATE: 22-JUL-1991
ATTORNEY/AGRNT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               1 tatagggcacgcgtggtcgacggcccgggctggtactggga 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 tatagggcacgcgtggtcgacggcccgggctggtactgaga 43
                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 33229/164/PIHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                             Score 39.4;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suite 500
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Patent No. 5426041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                             1.78;
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 97.00,
"when 40; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: double
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                          ; ORGANISM: Mus musculus US-09-570-367C-1
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ZIP: 20007-5109
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LOCATION:
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                                                                                                                                                                                                                             DNA
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Pred. No. 2.5;
Sequence 1, Application US/09570367C Patent No. 6338851
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.7%;
Best Local Similarity 44.5%;
Matches 286; Conservative
                                                                                                                                                                           LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE: NO
US-08-487-826B-13
                                                                                                                                                                                                                                                                MOLECULE TYPE:
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    ; ORGANISM:
US-08-998-416-472
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                                                                                                                                                                                             6851 TCTTACGTAAATTTATTTGATATTTTTAACTAATTTTATATATTTTATGCTTTTCCAAT 6910
                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Philippsen, Peter
APPLICANT: Philippsen, Rainer
APPLICANT: Poblmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Monty Ciristine
APPLICANT: Wendland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rebisching, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                 DB 1; Length 8585;
                                               Score 39.2; DB 1; Length 8 Pred. No. 2.1; 0; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
1919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATYORNEY_AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30:
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 472, Application US/08998416 Patent No. 6239264
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INFORMATION FOR SEQ ID NO: 472:
SEQUENCE CHARACTERISTICS:
LENGTH: 767 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                             Query Match 1.7%;
Best Local Similarity 50.0%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                      1893 acaattttgcatatca 1908
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ORIGINAL SOURCE:
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US-08-998-416-472/c
US-08-030-096-3
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                                                                                                                                          510 AGGTAAATTTAGTAGGTAGTAATATCCAATTAAAGGGAGACTATTAAATAGAAATAT 451
                                                                                                                                                                                                                                               GENERAL INCORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REPERENCE: 210121.45501
CURRENT PILLING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: 09/40,802
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 100
LENGTH: 583
                                     ;
0
   Length 767;
Score 38.6; DB 4; Length 7
Pred. No. 0.87;
0; Mismatches 104; Indels
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OTHER INFORMATION: Where n is
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LOCATION: (548)
OTHER INFORMATION: Where n is
NAME/KEY: modified_base
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uvery Match 1.7%;
Best Local Similarity 49.3%;
Matches 101; Conservative (
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OTHER INFORMATION: Where
NAME/KEY: modified_base
LOCATION: (538)
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LOCATION: (506)
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ORGANISM: Homo sapiens
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; NAME/KEY: promoter
; LOCATION: (1)..(2361)
US-09-561-825-26
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US-09-561-825-27/c
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                                                                                                                                                                                                                                                                                                 1758 ggaaaaaaaagattttggttgagactaaattactcatcgtcaaaataatgtcaaaatagtt 1817
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                                                                                                                                                                              Gaps
                                                                                        Score 38.2; DB 4; Length 583;
Pred. No. 0.97;
0; Mismatches 143; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ISHIGE, Fumiharu
APPLICANT: WATANABE, Eijiro
APPLICANT: WATANABE, Eijiro
APPLICANT: OEDA, Kenji
ITILE OF INVENTION: PLANT PROMOTERS
FILE REFERENCE: 2185-0431P
CURRENT APPLICATION NUMBER: US/09/561,825
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: JP 11-124527
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 30
                      or
                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Glycine max cv. Williams 82
; LOCATION: (569); OTHER INFORMATION: Where n is a, c, US-09-123-912-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-561-825-1/c
; Sequence 1, Application US/09561825
; Patent No. 6337430
                                                                                      Query Match 1.7%;
Best Local Similarity 48.4%;
Matches 140; Conservative
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US-09-561-825-1
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REBUILT 14

08-09-561-82-16/c

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us-09-807-470-3.rni
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Search completed: September 6, 2002, 15:18:39 Job time: 7823 sec

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% Search time 3580.18 Seconds
(without alignments)
8625.553 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                       13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                       6, 2002, 13:07:54
                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                          IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                         US-09-807-470-3
2288
                                                                                                                       September
                                                                                                                                                                                                                             Perfect score:
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                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                       Searched:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : EST:\*
1: em\_estha:\*
2: em\_esthum:\*
3: em\_estin:\*
4: em\_estin:\*
5: em\_estpv:\*
6: em\_estpv:\*
7: em\_estpv:\*
10: gb\_est1:\*
10: gb\_est2:\*
11: gb\_gss:\*
11: gb\_gss:\*
13: em\_gss\_hum:\*
14: em\_gss\_pln:\*
15: em\_gss\_pln:\*
16: em\_gss\_pln:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 29 Row: h Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF

analysis

.         18         481.8         21.1         769         10         BG542329           19         481.8         21.1         808         10         BI830439           20         472.         20.6         60         10         BI830439           21         472.         20.6         60         10         BI830439           22         462.         20.5         969         10         BG975574           23         462.         20.2         1015         10         BG975574           24         453         20.2         10         BG975574           25         459         20.1         695         10         BG975574           26         453.6         19.8         10         BG74881           26         453.6         19.8         651         10         BG714881           27         453         19.8         651         10         BG714881           28         476         9         AII333351         BG714881           29         477.2         19         BG323304           44         19.4         10         AG0         BG714881           31         44
18     481.8     21.1     769       20     476.20.8     496       21     472.2     60.8     496       22     468.20.5     969       23     462.8     20.2     1015       24     452.8     20.2     1015       25     453.6     19.8     651       26     453.6     19.8     651       29     447.2     19.4     450       31     444.1     19.4     450       34     442.8     19.4     460       34     442.8     19.4     608       35     436.8     19.1     944       37     433.6     19.0     494       40     426.6     18.9     835       40     426.6     18.9     835       40     422.8     18.5     736       41     423.8     18.5     736       42     42.1     18.4     1048       43     418.4     118.3     773       44     418.4     118.3     773       45     418.4     118.3     773       45     418.4     118.3     773
481.8 21.1 21 481.8 21.1 22 472.7 20.6 22 468 20.8 23 462.8 20.2 24 459 20.1 25 459 20.1 26 453.6 19.8 451.8 19.7 447.2 19.5 447.2 19.5 447.2 19.5 447.2 19.4 31 444.8 19.4 32 444.8 19.4 34 442.8 19.4 35 436.8 19.1 442.8 19.4 36 433.6 118.9 442.8 19.4 37 432.6 118.9 444.8 19.4 38 436.8 19.1 442.8 19.4 442.8 19.4 442.8 19.4 442.8 19.4 443.6 118.9 444.8 19.4 444.8 19.4 445.8 19.6 432.6 118.9 432.6 118.9 433.8 118.5 444.8 118.5 444.8 118.5 445.8 118.5 446.6 118.5 447.8 118.5 448.8 118.5 448.8 118.5 449.8 118.5 449.8 118.5 449.8 118.5
481.8 481.8 20 476.2 22 462.8 24 462.8 25 462.8 462.8 26 463.6 27 47.2 28 47.2 31 444 32 444 33 444 34 444 444 34 444 444 34 444 34 444 444 34 444 444 34 444 444 34 446 447 447
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## ALIGNMENTS

bp mRNA linear HTC 20-DEC-2001 19858, mRNA.	Homo sapiens Bukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 3 (Lasses 1 to 1356)	Differ Summission Submitted (20-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	USH-MGC Project URL: http://mgc.ncl.nih.gov Contact: MGC help desk Emall: gapbs-r@mall.nih.gov Contact: MGC help desk Emall: gapbs-r@mall.nih.gov Contact: DCTD/DTP CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing Center Center code: B#CM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: villalon@bcm .tmc.edu. Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M.,Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gunaratne, P., Yoon, V., Kowis, C., Martin, R., Lawrence, S., Richards, S., Gibbs, R.A.
1 3 BC020283 1356 bp ION Homo sapiens, clone IMAGE:4519858, NN BC020283 BC020283.1 GI:17946782 S HTC.	Σ	_	
RESULT 1 BC020283 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	ORGANISM ORGANISM REFERENCE AUTHORS	JOURNAL	REMARK COMMENT

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SOURCE
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TITLE
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                                                                                                                      DB 11; Length 1356;
match
                                                   adenocarcinoma."
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5' EST
                                                                                                                     34.3%; Score 785.8; DB 11; 79.2%; Pred. No. 2.6e-150; live 0; Mismatches 242;
 ou
clone has the following problem:
Location/Qualifiers
1. .1356
                                                                           /note="Vector: pcMV-SPORT6"
279 c 268 g 408 t
                  1. 1356
/organism="Homo sapiens"
/db_xref="taxon:9506"
/clone="INAGE:4519858"
/tissue_type="Prostate, ac/clone_lib="NIH_MCC_91"
/lab_host="DH10H_MCC_91"
                                                                                                                              Similarity 79.2
89; Conservative
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This
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Matches 98
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/note="Organ: brain; Vector: pBluescriptR (modified bBluescript KS+); Site_1: BamHI; Site_2: Sall-KNDI (gtcgag bBluescript KS+); Site_1: BamHI; Site_2: Sall-KNDI (gtcgag ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTTTTV3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG714759 760 bp mRNA linear EST 08-MAY-2001
602673845F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4796626 5',
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Primates; Catarrhini; Hominidae; Homo.
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Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shirah Toshiyuki and Piero Carninci (RIKRN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
Clone distribution: MCC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                  1024 AATTITCAGCTICGAAGGIGGAGGAACATICIGCTITICAGGCACCAGCIGIGAAGAAG 1083
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NIH WGC http://mgc.nci.nih.gov/.
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_96"
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BASE COUNT ORIGIN

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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotL-oligo(dT) primer: Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 by Life Technologies. Contact: Feng Liang Life Contact Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Prochoologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 Http://fulllength.invitrogen.com" 2 others
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1064)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Eyll-length cDNA libraries and normalization
Unpublished (2001)

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EWRY cedex - France
BP 191 91006 EWRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 692.6; DB 9;
Pred. No. 2.9e-131;
0; Mismatches 209;
                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                         /sex="male"
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 constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." 191 c 191 g 199 t
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Pred. No. 2.1e-132;
0; Mismatches 3;
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5', mRNA sequence.
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S NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: capabs-refmail.nih.gov

Tissue Procurement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

Clone distribution: MGC Clone distribution information can be http://image.linl.gov

Plate: LLAM12239 row: 1 column: 17

High quality sequence stop: 723.
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DH10B (phage-resistant)"
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Site_2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library." 3 others
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                                                                                                                        ggaagcgccaccatggggctccgtaagaagagcaccaagaaccccccgttctcagccag 524
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                                                                                        Length 1142;
                                                                                 Score 608.2; DB 10; Length
Pred. No. 5.1e-114;
0; Mismatches 154; Indels
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ilarity 82.0%;
Conservative (
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AU130188 AZ PP MRNA linear EST 24-OCT-2000 AU130188 NT2RP3 Homo sapiens cDNA clone NT2RP3000388 5', mRNA
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/clone_lib="NT2RB3"
/cell_lipe="Letatocarcinoma"
/cell_line="NT2"
/note="Vector: pME189FL3; mRNA from NT2 neuronal precursor
/cells after 2-weeks retinoic acid (RA) induction"
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 822)
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.
                                                                                                                                                                                                                                                                                                  Ota, T., Nishikawa, T., Suzuki, Y., Ishli, S., Saito, K., Kawal, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
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Contact: Takeo Isogai
Contact: Takeo Isogai
Contact: Takeo Isogai
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Fax: 81-438-52-3951
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/db_xref="taxon:9606"
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/note="Corgan: testis; vector: pcNv-SPORT6; Site_1: NotI;
Site_2: Sali; cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb Library enriched for full-length clones and constructed by Life Technologies.
full-length clones and constructed by Life Technologies.
to 259 c 241 g 349 t lothers
                                                                                                                                                                                                                                                                                                                Contact: Rolert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.W.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 GTCACCCTCCCAGCAACAAGAACAAGCTACTGAATCAGTGTCCCTTTATTACTATGGC 280
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1135)
NHH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Location/Qualifiers
                                                                                                                  BM466239.1 GI:18515281
                                                                    5', mRNA sequence.
BM466239
                                                                                                                                                                                 Homo sapiens
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                    Isogai,T.
HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y.,
Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano
J.S., Masuho,Y., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                    Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1632-3 Yana, Kisarazu, Chiba 292-0812, Japan
1638-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Pred. No. 8.8e-103;
0; Mismatches 136;
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24.2%;
Best Local Similarity 82.4%;
Matches 645; Conservative
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CDNA clone NT2RP4000757 5', mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(Dases 1 to 814)
Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
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                                          Length
                                                                                     Indels
                                                                                     0; Mismatches 140;
                                          DB 9;
                                                                 Pred. No. 3.4e-103
                                          Score 555.2;
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AU132871 NT2RP4 Homo sapiens
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AU132871
AU132871.1 GI:10993410
                                          24.3%;
82.0%;
                                                                                     Matches 638; Conservative
                                                                 Similarity
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Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Euto779)

En (bases 1 to 779)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LinL at:

http://inage.llnl.gov

Plate: LCM1942 row m column: 13

High quality sequence stops: 778.
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//tissue_type="carcinom, cell line"
//tab_host="https://tab.nostate; vector: potral;"
//note="Organ: prostate; vector: potral; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dr priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Strategene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                    BM045930 779 bp mRNA linear EST 07-NOV-2001 603624955F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5451828 5',
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                             1065 cttgtctacattggtcttcacctcttccacattactggagcttatcttgtacttgaat 1124
                                                                                                 catttgggacttcttcttttggtactgcattattttgttgaattactttcccacatgtgc 1184
                                                                                                               CTTCATGCTTTTCCTGAACTCTACTTCCAGAAAACCAAAAAGAAGAAGATATTCCTCGTCAG 632
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Pred. No. 1.7e-98;
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_40"
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BM045930.1 GI:16775197
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83.8%;
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TITLE
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BE612552 790 bp mRNA linear EST 20-OCT-2000 601452065F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855665 5', mRNA sequence.
BE612552.1 GI:9894149
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I (bases 1 to 790)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                      747 atcattattcatgccacaattcaggaatatgtgttggataaaattaacaagagaatgcag
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ctcactcttcagcacagtgttgctgtccctgcagcagaggaacaagccacgggctcaaag
                                                                                                                                                                                                                                                         181 ATAATTATTCATGCCGTAATTCAAGAGTATATGTTGGATAAAATTAACAGGCGAATGCAC
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BI870787.1 GI:16044460
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/organism="Romo sapiens"
/drams="Romo sapiens"
/drams="IMAGE:385565"
/clone=lib="NIH_MGC_66"
/clone=lib="NIH_MGC_66"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: owary; Vector: pCMY-SPORT6; Site_1: Not1;
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/site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
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Pred. No. 3.1e-94;
0; Mismatches 112; Indels
cound through the I.M.A.G.E. Consortium/LLNL at:
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Plate: LLAM9583 row: b column:
                                 High quality sequence stop: 669
Location/Qualiflers
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Best Local Similarity 83.8%;
Matches 578; Conservative (
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 879)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BI870787 879 bp mRNA linear EST 11-OC
603394607F1 NIH_MGC_90 Homo sapiens CDNA clone IMAGE:5404608
                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnl.gov
Plate: LLAM12031 row: n column: 01
High quality sequence stop: 820.
Location/Qualifiers
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Pred. No. 7.9e-94;
0; Mismatches 161; Indels
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/clone="IMAGE:5404608"
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Contact: Takao Isogai
Contact: Takao Isogai
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
152-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3953
Fax: 81-438-52-3953
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix Research Institute of Medical Science, University of Tokyo, and Helix Research Institute.
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/cell_type="teratocarcinoma"
/cell_line="wizer"
/note="vector: pWE18SFL3; mRNA from NT2 neuronal precursor
/note="vector: pweks retinoic acid (RA) induction"
cells after 2-weeks retinoic acid (RA) induction"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 905)
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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                                                                              1000 actggtttcatgcttttcctgaactctac-ttccagaaaaccaaaaaaaaagacatccct
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/db_xref="taxon:9606"
/clone="NT2RP3002413"
/clone_lib="NT2RP3"
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AU131342.1 GI:10991696
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602573813F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4702154 5', mRNA sequence.
BG547017
BG547017.1 GI:13545682
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                      705 gtcaaagatttggccacggttttcttctacatgctggtggcaatcattattcatgccaca
Length 905;
DB 9;
         1.4e-93
                    0; Mismatches
Score 508.2;
Pred. No. 1.4
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NIH-MGC http://mgc.nci.nih.gov/.
22.2%;
81.8%;
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mRNA sequence.
BF969571
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/lab_host="DHIOB (TI phage-resistant)"
/note="Organ: lung; Vector: pDRN-LIB (Clontech); Site_l:
Sfil (gqccgctcgqcc); Site_l: Sfil (ggccattatgqcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-ARCGGCCATATGGCC.3' and 3' adaptor sequence:
5'-ARTCTAGAGGCCGAGCAGCCGCAGCTGTGT(3)DN+3' (where B = A,
C, or G and N = A, c, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MC Library."
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Lupublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs rémail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayad by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCALISS row: i column: 03
High quality sequence stop: 714.
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Best Local Similarity 84.0%;
Matches 604; Conservative C
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dclone="inAdE:43606"
/clone=lib="NH-MGC_84"
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/lab_host="NH108 (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
NotI: Site_2: Sall; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
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Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMN0000 row: 1 column: 06
High quality sequence stop: 672.
1. 836
                                 29 GCCGCCCCACCATGGCGATTCGCAAGAAAGCACCACAAGAGCCCCCCAGTGCTGAGCACCAC
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80.7%; Pred. No. 5e-92;
.ive 0; Mismatches 139; Indels
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211 c 176 g 252 t
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates;
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/cell_line="NT2"
/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 2 weeks retinoic acid (RA) induction"
1 169 c 150 g 300 t 13 others
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP2003491"
/clone_lib="NT2RP2"
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Contact: Tako Isogai
Contact: Tako Isogai
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Contact: Tako Isogai
Contact: Tako Isogai
Contact: Tako Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana. Kisarzau, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hrl.co.jp
HRI human cDNA project; 5- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology. Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
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AUTHORS
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Length 879;
                   Indels
Query Match 21.7%; Score 497.4; DB 9; Best Local Similarity 77.7%; Pred. No. 2.2e-91; Matches 620; Conservative 0; Mismatches 175;
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/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Ab_ref="Haxon:9606"
/ Clone="IMAGE:534104"
/ Clone=lib="NIH_MGC_71"
/ Lissue=Lype="lelomyosarcoma"
/ Lab_host="DH10B" (phage-resistant)"
/ Note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
/ Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
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                                                       BM459490 910 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6417971 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534104
                                                                                                                                                                                                                                             Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

(Dases 1 to 910)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.a column: 17
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82.2%; Pred. No. 6.3e-91;
tive 0; Mismatches 128; Indels 6;
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                                                         1179 atgtgcggcctgttttactttagtgatgaaaa 1210
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Search completed: September 6, 2002, 13:08:10 Job time: 46629 sec

us-09-807-470-4.rag

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

; Search time 74.4 Seconds 6, 2002, 17:09:47 September Run on:

(without alignments)
550.890 Million cell updates/sec

369

US-09-807-470-4 1920 1 MGLRKKSTKNPPVLSQEFIL.....VGVETSNRVDCPPKRKEKSS Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

747574 seqs, 111073796 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:\*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:\* A\_Geneseq\_032802:\*

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4: /SIDSI/gcgdata/hold-geneseqp-embl/AAl983.DAT:
5: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AAl983.DAT:
6: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AAl983.DAT:
7: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AAl986.DAT:
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9: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AAl996.DAT:
9: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AAl996.DAT:
9: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AAl999.DAT:
9: /SIDSI/gcgdata/hold-ge 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Human WAR-1 amino	Novel human diagno	Human WAR-1 protei	Human polypeptide,	Rat WAR-1 amino ac	Rat WAR-1 protein	Human cancer assoc	Human prostate can	Human reproductive	Drosophila melanoq	Drosophila melanog
10	AAY98147	ABG12234	AAB70695	AAM93265	AAY98146	AAB70696	AAB43601	AAY48434	AAM95708	ABB65847	ABB66114
DB	21	22	22	22	21	22	21	20	22	22	22
Length	369	369	369	369	363	363	416	304	384	368	368
Query e Match Length DB I	100.0	100.0	100.0	6.66	76.2	76.2	72.5	58.8	42.4	31.4	31.4
Score	1920	1920	1920	1919	1463	1463	1392.5	1129.5	815	602.5	602.5
Result No.		2	m	4	ស	Q	7	80	σ	10	11

Drosophila melanog Human secreted pro	Saccharomyces cere	Human LAPH-1 prote	Human protein SEQ	Human protein sequ	Human secreted pro	Arabidopsis thalla	Human polypeptide	Human protein SEQ	Arabidopsis thalia	Arabidopsis thalia	Human LAPH-2 prote	Human hydrophobic	Arabidopsis thalia	Novel signal trans		Novel signal trans	Human olfactory re	E. coli cellular p	Group B Streptococ	Human secreted pro	Human apoptosis pr	Human glycine tran	Glycine transporte	Human neurotransmi		Human EST encoded	Human GLYTLIKE pro	Human GLYTLIKE pro	Novel human diagno	Zea mays protein f	Novel human diagno	Drosophila melanog
62	10	92	60	84	68	79	28	93	97	96	77	09	80	01	90	92	92	64	39	38	82	36	65	35	90	17	43	44	14	04	27	89
ABB67362 AAG00189	AAR86810	AAY00876	AAM78909	AAB93884	AAB24489	AAG41779	AAM42028	AAM79893	AAG44197	AAG44196	AAY00877	AAB88560	AAG41780	AAU17201	AAB43806	AAU17576	AAG72076	AAU34864	AAY27339	AAB34938	AAU00782	AAB35236	AAB47065	AAB35235	ABB60006	AAM23517	AAY81943	AAY81944	ABG25514	AAG33404	ABG29227	ABB66068
22 21	17	20	22	22	21	21	22	22	21	21	20	22	21	22	21	22	22	22	20	21	22	22	22	22	22	22	21	21	22	21	22	22
1575	411	394	394	394	191	310	488	536	280	296	380	380	254	181	266	158	332	484	816	150	311	692	638	692	339	414	642	642	1898	313	577	262
31.4	7.5	7.4	7.4	7.4	7.2	9.9	6.1	6.1	6.1	6.1	6.0	0.9	•				5.5			•	5.3		5.3	5.3	5.2	5.2	5.2	5.2		5.2	5.1	5.1
602.5	144	143	143	143	138	127	117.5	117.5	116.5	116.5	116	116	115	114.5	114	113	106.5	105.5	105.5	104.5	102	102	101	101	100.5	100	100	100	100	99.5	98.5	97.5
12	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Endoplasmic reticulum; WAR-1; cancer cell proliferation inhibitor; diagnosis; cancer; sarcoma; human. AAY98147 standard; Protein; 369 AA Human WAR-1 amino acid sequence. 99WO-JP05631. 98JP-0290711. (first entry) WO200022123-A1 Homo sapiens 13-OCT-1999; 13-OCT-1998; 22-AUG-2000 20-APR-2000 AAY98147; П AAY98147 RESULT 

Tojo S, Nemoto K, Ishikawa H; Komiya K, (SUMU ) SUMITOMO PHARM CO LTD Tohdoh N, Yoshima T, Okuyama H;

WPI; 2000-317980/27. N-PSDB; AAA38013 Endoplasmic reticulum protein WAR-1 which inhibits cancer cell proliferation for use in treatment and diagnosis of cancer including sarcomas of high malignancy -

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Tang YT;

Liu C,

RT,

Drmanac

2001-639362/73

N-PSDB; AAS76421

Claim 20; SEQ ID No 42593; 103pp; English.

biodiversity

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                                      This sequence represents an endoplasmic reticulum protein (WAR-1) amino acid sequence. The invention includes rat and human WAR-1 sequences, expression vectors containing the DNA, cells transformed with the expression vector, antibodies against WAR-1, and probes and primers which hybridise to the DNA encoding WAR-1. The WAR-1 protein inhibits the proliferation of cancer cells, and is used in the treatment and diagnosis of cancers including highly malignant sarcomas.
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                                                                                                                                                                                                 Length 369;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                     / Match 100.0%; Score 1920; DB 21;
Local Similarity 100.0%; Pred. No. 2.7e-214;
nes 369; Conservative 0; Mismatches 0;
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              2; 89pp; Japanese.
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                   369 AA;
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            Claim 1; Fig
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) are useful in medical cinsorders involving partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical cinsorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cid sequences ABG00010-ABG30377 represent novel human constitution, but was obtained in electronic format directly from WIPO very
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100.0%; Pred. No. 2.7e-214;
Live 0; Mismatches 0;
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AAB70695 standard; Protein; 369 AA.

us-09-807-470-4.rag

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Sat

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The present invention describes a screening method for secretory and membrane proteins consisting of transformation of a cell with separate expression vectors for the sense and antisense RNA of DNA encoding an endoplasmic reticulum membrane protein participating in endoplasmic reticulum transport of proteins. Also described are: (1) secretory and cell membrane proteins identified by the screening method; (2) drug compositions containing these proteins; (3) host cells transformed by the separate expression vectors of the method; and (4) the preparation of secretory and cell membrane proteins by culture of the transformants. The method can be used for the identification and preparation of proteins for use in the treatment and prevention of diseases such as cancer, disorders of the nervous system, immune disorders (including allergies and rheumatism) and skeletal disorders. The present sequence in the transformed human WAR-I protein from the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Nemoto K;
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Pred. No. 2.7e-214;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ishikawa H,
                                                                                   Human WAR-1 protein sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 58-60; 79pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Imamura
                                                                                                                                                                                       rheumatism; skeletal disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins expressed by the cell
                                                                                                                                                                                                                                                                                                                                                                                               (SUMU ) SUMITOMO PHARM CO LTD.
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Best Local Similarity 100.0%;
Matches 369; Conservative 0,
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                                                 (first entry)
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                                                 17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
                 AAB70695;
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA assily encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                            360
                                                                                                                                                           FSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAKIAV 300
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                               LSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKKRSRSSKKRTENGVGVETSNRVDC
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 3.5e-214;
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2000JP-0118774.
2000JP-0183765.
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|ppkrkekss 369
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11-JAN-2000;
02-MAY-2000;
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                                       Matches 279;
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Sequence
                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endoplasmic reticulum protein WAR-1 which inhibits cancer cell proliferation for use in treatment and diagnosis of cancer including
                                                                                                                                                    Endoplasmic reticulum; WAR-1; cancer cell proliferation inhibitor;
ESGQFSVFYFFSCIWGTF1L1SENCLSDPTL1WKARPHSMMTFQMKFFY1SQLAYWFHAF
                                                               FSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAKIAV
                                                                                                                              AAEEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFN
                                                                                       PELYFQKTKKQDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFY
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                                                                                                                                                                                                                                                                                                                  diagnosis; cancer; sarcoma; rat
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                                                                                                                                                                                                                                                                                         Rat WAR-1 amino acid sequence.
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sarcomas of high malignancy
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                                                                                                                                                                                             PPKRKEKSS 369
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Okuyama H;
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                                    Gaps
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                                                                      1 MGLRKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVP
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Length 363;
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                                      40;
Score 1463; DB 21;
Pred. No. 3.7e-161;
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                                    43; Mismatches
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76.2%;
75.8%;
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                                      Conservative
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                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 PPKRKEKS 368
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neurological disease; drug screening

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The present invention describes a screening method for secretory and membrane proteins consisting of transformation of a cell with separate membrane proteins consisting of transformation of a cell with separate expression vectors for the sense and antisense RNA of DNA encoding an endoplasmic reticulum membrane protein participating in endoplasmic reticulum transport of proteins. Also described are: (1) secretory and cell membrane proteins identified by the screening method; (2) drug compositions containing these proteins; (3) host cells transformed by the separate expression vectors of the method; and (4) the preparation of secretory and cell membrane proteins by culture of the transformants. The method can be used for the identification and preparation of proteins for use in the treatment and prevention of diseases such as cancer, disorders of the nervous system, immune disorders (including allergies and rheumatism) and skeletral disorders. The present sequence invention is a specifically claimed rat WAR-1 protein from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiarthmatic; antiarthmitic; antidiamatory; antithyroid; antilallergic; antidacterial; antidiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAEEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESGQFSVFYFFSCIWGTFILISENCLSDPTLIWKARPHSMMTFOMKFFYISOLAYWFHAF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PELYFQKTKKQDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKKRSRSSKKRTENGVGVETSNRVDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cancer associated gene; cancer antigen; detection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.2%; Score 1463; DB 22; Length 363; 75.8%; Pred. No. 3.7e-161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cancer associated protein sequence SEQ ID NO:1046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43; Mismatches
Claim 3; Page 60-62; 79pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB43601 standard; Protein; 416 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPKRKEKS 368
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355 ppkkkeka 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
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AAB43601
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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB4239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antithyroid; antiarthritic; antidiabetic; antiasthmatic; antithyroid; antidiabetic; antiasthmatic; antithyroid; antidiabetic; coagulant; carmatological; neuroprotective; cardiant; thrombolytic; coagulant; noctropic; vasotropic; antipsoriatic and antiangiogenic. The noctropic; vasotropic; antipsoriatic and antiangiogenic. The coagulant; noctropic; vasotropic; antipsoriatic and antiangiogenic andiorating medical conditions and diagnosing pathological conditions. Coagulant; not medical conditions and integration pathological conditions. Coagulant; and integrating or inhibiting the proliferation of fiferentiation or mobilisation of immune cells, to treat disorders of haematopotetic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The petrological disease and bacterial or viral infections. The petrological disease and chargonists and antagonists may be also be used in drug screens. AAC78451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AAEEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGLRKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVP 60
                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:|||||| ||||::|:||||:|||:|||||||| ||| :|| | ||| |||| :||| fsnekygkgfslwavlfvlgrlltlilsvltvgfglaraengkldfstgnfnvlavriav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESGQFSVFYFFSCIWGTFILISENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAKIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PELYFQKTKKQDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.5%; Score 1392.5; DB 21;
71.4%; Pred. No. 7e-153;
.ive 44; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 1634-1636; 2352pp; English.
                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                         99US-0124270.
                                                                                                                                                     2000WO-US05882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.4<sup>§</sup>
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention.
                                                                                                                                                                                                                                                                      Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                           2000-587533/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 AA;
                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAC77810
                                                                          WO200055350-A1
                                      Homo sapiens.
                                                                                                                                                     08-MAR-2000;
                                                                                                                                                                                         12-MAR-1999;
                                                                                                               21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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AAY48434

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Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                      QDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFYFSDEKYQKGI
                                                                            SLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAKIAVLSSSCTIQAY
                                                                                                                                                                                                                                                                                                                                                                                                           Human reproductive system related antigen SEQ ID NO: 4366.
                                                                                                                                                                                                                                                                                                              AAM95708 standard; Protein; 384 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2001; 2001WO-US01339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0186350
2000US-0189874
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                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; qene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
                                                                                                                                                                                                    366 EKSS 369
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14-JUL-2000;
26-JUL-2000;
                                                                                                                                                                                                                                   301 ekss 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUL-2000;
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14-AUG-2000;
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22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                            21-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-2001
                                                                                                                                                                                                                                                                                                                                             AAM95708;
                191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed at high level in normal prostatic tissue. Polypeptides (1) encoded by (A) are used: (a) for identifying agents for treatment of prostatic cancer and (b) for therapy of prostatic cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (1), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before these are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTs. AAV48304-Y48456 represent peptides encoded by the expressed sequence tags described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid expressed at high level in normal prostatic tissue and encoded polypeptides, used to treat cancer and screen for therapeutic
                                                                                                                                                                                                                                                                                              Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy; cancer; tissue specificity; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosenthal A;
                301 LSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKK----RSRSSKKRTENGV-GVETS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNESGQFSVFYF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 FSCIWGTFILISENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel nucleic acid sequences (A) that are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20; Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.8%; Score 1129.5; DB 2 70.7%; Pred. No. 1.7e-122; ive 35; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ပဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schmitt A, Pilarsky
                                                                                                                                                                                                                                                                  Human prostate cancer-associated protein 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                     AAY48434 standard; Protein; 304 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; 174; 194pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                        98DE-1011194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98DE-1011194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.8%.
Best Local Similarity 70.7%.
Matches 215; Conservative
                                                                                                                                                                                                                                   (first entry)
                                                            356 NRVDCPPKRKEKSS 369
                                                                               1 | | :|||||
403 nvadsprnkkekss 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Specht T, Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-519629/44.
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PR 17-NOV-2000; 2000US-0249211.

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PR 17-NOV-2000; 2000US-0249215.

PR 17-NOV-2000; 2000US-0249215.

PR 17-NOV-2000; 2000US-0249215.

PR 17-NOV-2000; 2000US-0249216.

PR 17-NOV-2000; 2000US-0249216.

PR 17-NOV-2000; 2000US-024924.

PR 17-NOV-2000; 2000US-024929.

PR 05-DEC-2000; 2000US-024929.

PR 06-DEC-2000; 200US-024929.

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LYFQ -- KTKKQDIPRQLVYI -GLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLF

240 --YFSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAK

GOFSVFYFFSCIWGTFILISENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPE

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298 IAVLSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKKRSRSSKKRTENGVGVETSNR

291 llalgglialggylvfsfit----

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337 aktpkdkvkrkkes 350

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                   | | | ||:: | | | |: | | | |:| |310 lllvcaaqawlmwrfihsqlrxwreywneqsa---krrvpatprlparlikresgyheng 366
                                                                                                                                                                                                                                                                                                      developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 24333.
LSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKR-
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11-JUL-2000; 2000US-0614150.
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                                                            350 VGVETSNRVDCPPKRKE 366
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Drosophila; developmental biology; cell signalling; insecticide;

Drosophila melanogaster

pharmaceutical

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27-SEP-2001.

23-MAR-2001; 2001WO-US09231. 23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150.

Drosophila melanogaster polypeptide SEQ ID NO 25134.

(first entry)

26-MAR-2002

ABB66114;

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ABB66114 standard; Protein; 368

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Length 368;

DB 22;

31.4%; Score 602.5; DB 22; 36.9%; Pred. No. 4.4e-61; ive 63; Mismatches 132;

Best Local Similarity 36.9 Matches 138; Conservative

Query Match

Indels

63 EEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNES 122 reqpygkpytyiagikdycaiffytltciimhaiiqefvldkiskklhlskfklarfnes 128

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4 RKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVA-VPAA 62 

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                                                                                                                 GQFSVFYFFSCIWGTFILISENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPE 182
                                                                                                                                                               63 EEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNES 122
                                                                                                                                                                                              LYFQ--KTKKQDIPRQLVYI-GLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLF 239
                                                                                                                                                                                                                                           240 --YFSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAK 297
                                                                                                                                                                                                                                                                                        298 IAVLSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKKRSRSSKKRTENGVGVETSNR 357
                                  Gaps
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                                  41;
           Length 368;
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                                 Indels
                                                                                                                                                                                                                                                                 247 gvfdreerlaklrvvnnavfflirfatsvigvltlyygiggvrs---
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         DB 22;
        Query Match 31.4%; Score 602.5; DB 22; Best Local Similarity 36.9%; Pred. No. 4.4e-61; Matches 138; Conservative 63; Mismatches 132;
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11-JUL-2000; 2000US-0614150.
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337 aktpkdkvkrkkes 350
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N-PSDB; ABL11465.
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                                                                    sequences (ABL01840-ABL16175) and the encoded proteins (ABB7737-ABB72072).
(ABB57737-ABB72072).
Specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
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                                                                                                                                                                                                                     31.4%; Score 602.5; DB 22; 36.9%; Pred. No. 3.6e-60; iive 63; Mismatches 132;
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Matches 138; Conservative
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|1544 aktpkdkvkrkkes 1557
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                                                                                                                                                                                                   The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                               diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGLRKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVP 60
                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21; Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae; LAG1; life-span limiting domain; life-span extending domain; stress tolerance; longevity; recombinant protein production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.7%; Score 493; DB 21; Length 1 Best Local Similarity 76.6%; Pred. No. 5e-49; Matches 95; Conservative 15; Mismatches 14; Indels
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194..411
                                                                                                                                                             Claim 13; SEQ ID 4270; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae LAG1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR86810 standard; Protein; 411 AA.
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94US-0253875
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2000-500381/45.
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                       N-PSDB; AAC00195
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Longevity-assurance protein homologue; LAPH-1; human; cell proliferation; longevity-assurance protein homologue; LAPH-2; signal transduction; cell cycle regulation; apoptosis; cellular homeostatic pathway; aging; cancer; inflammation; autoimnume disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         itfitfirefimdvvirpftvylnvtsehrqkrmleqmyaifycgvsgpfglyimyhsdlw 200
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261 lliwssyvfhftkmglaiyitmdvsdfflslsktlnylnsvftpfvfglfvffwiylrhv 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNESGQFSVFYF-FSCIWGTFILI-SENC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 FFLLGLVFEGTAEASIVFLTLQHSVAVP-----AAEEQATGSKSLYYYGVKDLATVFFYM 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    life-span limiting domain (see AAR86812) and a life-span extending domain (see AAR86812) and a life-span extending domain (see AAR86811). Overexpression of the LAG1 gene in older cells has a rejuvenating effect, which not only increases replication and so reproductive capacity and cellular tolerance to stress factors such as starvation and low pH. These cells may be used for the production of recombinant proteins. By increasing the life span of recombinant cells, the need for overexpression of recombinant gene products is avoided, and therefore any subsequent adverse effects on the host cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 FHITGAYLLYLNHLGLLLLV-------LHYFVELLS-HMCGLFY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae LAG1 gene product is composed of a
                                                                                                                                                                                                                                                 Eukaryotic LAG1 gene and protein - controls longevity, stress tolerance and reproductive capacity of eukaryotic cells, for improved prodn. of recombinant proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%; Score 144; DB 17;
22.6%; Pred. No. 1.1e-07;
tive 49; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                        Claim 23; Page 100-102; 154pp; English.
(RESE ) RESEARCH CORP TECHNOLOGIES INC
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                                                                                                                                                                               N-PSDB; AAT07263
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                                                                     Jazwinski SM;
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11-FEB-1999

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This sequence is the human longevity-assurance protein homologue of
the invention, designated LAPH-1. LAPH-1 and LAPH-2 are involved in
signal transduction and cell cycle regulation, and may play a role in
regulating the balance between cell proliferation and apoptosis.

Increased expression of LAPH-1 or LAPH-2 may increase susceptibility to
disregulation of cellular homeostatic pathways. Antagonists of LAPH-1 or
LAPH-2 can be used to treat a disorder associated with disregulation of
cellular homeostasis or with aging, cancers, disorders associated
with inflammation or autoimmune disease including AIDS, Addison's
disease, adult respiratory distress syndrome, allergies, anaemia, asthma,
therosclerosis, bronchitis, cholecystitis, Crohn's disease, ulcerative
colitis, atopic dermatitis, dermatomyositis, diabetes mellitus,
colitis, atopic dermatitis, dermatomyositis, diabetes mellitus,
colitis, atopic dermatitis, dermatomyositis, diabetes mellitus,
colitis, atopic dermatitis, matchinia, irritable bowel syndrome,
colitis, atopic dermatitis, pancreatitis, rheumatoid arthritis,
costeoarthritis, osteoporosis, pancreatitis, rheumatoid arthritis,
costeoarthritis, syndrome, and autoimmune thyroidisis, infections,
neurodegenerative disorders including Alzheimer's disease, ammesia,
amyotrophic lateral sclerosis, bipolar disorder, catatonia, dementia,
depression, Down's syndrome, tardive dyskinesia, distonias, epilepsy,
Huntington's disease, multiple sclerosis, neurofibromatosis, Parkinson's
disease, schizophrenia, and Tourette's disorder, and myelodysplastic
                                                                                                                                                                                                                                                                                                  New isolated human longevity-assurance protein homologues - used to develop products for treating disorders associated with disregulation of cellular homeostasis or with ageing
                                                                                                                                                                                     Shah P;
                                                                                                                                                                                     Lal P,
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 1; 101pp; English.
                                                98WO-US15591.
                                                                                         97US-0902853.
                                                                                                                                       (INCY-) INCYTE PHARM INC
                                                                                                                                                                                     Corley NC, Hillman JL,
                                                                                                                                                                                                                               WPI; 1999-153788/13.
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                                              28-JUL-1998;
                                                                                         30-JUL-1997;
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228 FVELLSHMCGLFYFSDEKYQKGIS----LWAIVFILGRLVTLIVSVLTVGFHLAGSQNRN 283 108 RMOFTKAKONKFNESGQFSVFYFFSCIWGTFILISENCLSDPTLIWKARPHSMMTFQMKF 167 168 FYISQLAYWFHAFPELYFQKTKKQDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHY 227 ð g ð g ò g

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84; Indels 12; Gaps

7.4%; Score 143; DB 20; Length 394; 25.4%; Pred. No. 1.3e-07; ative 39; Mismatches 84; Indels 12

Query Match
Best Local Similarity 25.4%;
Matches 46; Conservative

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                                sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe sedineuroe 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08336031
Patent No. 5817782
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: LAG1: A GENE FOR INCREASING THE TITLE OF INVENTION: LONGEVITY OF EUKARYOTES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,031
US-09-213-398-3
US-07-741-453A-60
US-09-235-451-36
US-08-64-086-2
US-08-643-417-10
US-08-643-417-10
US-08-689-974-3
US-09-058-376-3
US-09-058-376-3
US-08-953-823A-5
US-08-953-823A-5
US-08-781-891-73
US-08-781-891-74
US-08-781-891-73
US-08-781-891-73
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US-08-781-891-73
US-08-781-891-73
US-08-072-064-8
US-08-072-064-8
US-08-072-064-8
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,875
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/POCKET NUMBER: 9303Z
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (516) 742-4343
TELEFAX: 230 901 SANS UR
TELEX: 230 901 SANS UR
SEQUENCE CHARACTERISTICS:
FEWSTH: 411 amino acids
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Matches 65; Conservative
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                                                                                                                                                                                                           6, 2002, 17:10:38; Search time 28.82 Seconds
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
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Compugen Ltd.
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PCT-US94-00198-2
US-08-510-284-1
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Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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201 LFKTKPMYRTYPVITNPFLFKIFYLGQAAFWAQQACVLVLQLEKPRKDYKELVFHHIVTL 260
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                   ---AAEEQATGSKSLYYYGVKDLATVFFYM
                                                                                            88 LVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNESGQFSVFYF-FSCIWGTFILI-SENC
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APPLICATION NUMBER: PCT/US95/06725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 9303Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELERAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                 33 FFLLGLVFEGTAEASIVFLTLQHSVAVP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
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STREET: 400 Garder
CITY: Garden City
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Best Local Similarity
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STATE: Ne
COUNTRY:
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88 LVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNESGQFSVFYF-FSCIWGTFILI-SENC 145
                                                                             146 LSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKKQDIPRQLVYIGL-HL 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Hillman, Jennifer L.

APPLICANT: Shah, Purvi

APPLICANT: Lal, Preeti

TITLE OF INVENTION: HUMAN LONGEVITY-ASSURANCE PROTEIN HOMOLOGS
NUMBER OF SEQUENCES: 7

CORRESPONDENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaccuticals, Inc.

STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
                                                                                                                                                                                                     205 FHITGAYLLYLNHLGLLLLV-------LHYFVELLS-HMCGLFY---
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                                                                                                                                                                                                                                                                                ----FSDEKYQKGISLWAIVFILGRLVTLI 266
                                                                                                                                                                                                                                                                                                    321 VNIRILMSVLTEFRHEGNYVLNFATQQYKCMISL-PIVFVLIAALQLV 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.5%; Score 144; DB 2; Le Best Local Similarity 22.6%; Pred. No. 3.7e-08; Matches 65; Conservative 49; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,853
FILING DATE: Herewith
CLASSIFICATION: ?
PRIOR APPLICATION: ?
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08902853
Patent No. 5945330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0;
TELECOMMULICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAS: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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CITY: Palo Alto
STATE: CA
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LIBRARY: General S41568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 411;
                                                                               LAG1: A GENE FOR INCREASING THE LONGEVITY OF EUKARYOTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,875 & 08/336,031
FILING DATE: 03-JUN-1994 & 08-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: DiG19110, Frank S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
Sequence 2, Application PC/TUS9506725
GENERAL INFORMATION:
APPLICANT:
TILE OF INVENTION: LAG1: A GENE FOR INCREASIN
TITLE OF INVENTION: LONGEVITY OF EUKARYOTES
NUMBER OF SEQUENCES:
CORRESPONDENCE SCUILY, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.5%; Score 144; DB 5; 22.6%; Pred. No. 3.7e-08;
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241 SSDYLLEACKMVNYM--QYQQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESIS-NRG 297
228 FVELLSHMCGLFYFSDEKYQKGIS----LWAIVFILGRLVTLIVSVLTVGFHLAGSQNRN 283
                                                               168 FYISQLAYWFHAFPELYFQKTKKQDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 SIVFLTLQHSVAVPAAE-----EQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Colley, Neil C.
APPLICANT: Shah, Puvoi A.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: HUMAN LONGEVITY-ASSURANCE PROTEIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OFFWARE: FASTEM: DOS SOFFWARE: FASTESO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/902,853 FILLIG DATE: Herewith CLASSIFITAMENTOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08902853
Patent No. 5945330
GENERAL INFORMATION:
APPLICANT: HILLMAN, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-O.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68; Conservative
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Best Local Similarity
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STATE: CA
COUNTRY: US
ZIP: 94304
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US-08-902-853-6
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US-08-902-853-6
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                  88 LVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNESGQFSVFYF-FSCIWGTFILI-SENC 145
                                                          141 IFFTFLREFLMDVVIRPFTVYLNVTSEHROKRMLEOMYAIFYCGVSGPFGLYIMYHSDLW 200
                                                                                                           LSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKKQDIPRQLVYIGL-HL 204
                                                                                                                                                   201 LFKTKPMYRTYPVITNPFLFKIFYLGQAAFWAQQACVLVLQLEKPRKDYKELVFHHIVTL 260
                                                                                                                                                                                                                                              261 LLIWSSYVFHFTKMGLAIYITMDVSDFFLSLSKTLNYLNSVFTPFVFGLFVFFWIYLRHV 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HIllman, Jennifer L.
APPLICANT: COTLEY, Neil C.
APPLICANT: Shah, Purvi
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
TITLE COF INVENTION: HUMAN LONGEVITY-ASSURANCE PROTEIN HOMOLOGS
CORRESPONDENCE: 7
CORRESPONDENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                               205 FHITGAYLLYLNHLGLLLLV------LHYFVELLS-HMCGLFY----
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                                                                                                                                                                                                                                                                                          -----FSDEKYQKGISLWAIVFILGRLVTLI 266
                                                                                                                                                                                                                                                                                                                 321 VNIRILMSVLTEFRHEGNYVLNFATQQYKCWISL-PIVFVLIAALQLV 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,853
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08902853 Patent No. 5945330
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LENGTH: 394 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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CLONE: 2516821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
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CITY: Palo Alto
STATE: CA
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16;

Gaps

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Length 380;

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Query Match
                                                         ---FHITGAYLLYLNHLGLLLL----VLHY--FVELLSHMCGLFYFSDEKYQKGISLWAI 255
                                                                                                                                                                                                                        247 GFNFLRVGNAILYIFDLSDYILSGGKMLKYLGFGKICDYLFGIF------VASWVY 296
                                                                                                                                                                                                                                                             256 V--FILGRLVTLIVS---VLTVGFHLAGSQNRNPDALTGNVNVLAAKIAVLSSSCTIQAY 310
                                                                                                                                                                                                                                                                                            297 SRHYLFSKILRVVVTNAPEIIGGFHL------DVPNGYIFNKPIYIAFIILLFTLQL- 347
78 AICFACLLSPSLRPYAEPFIFLSYKQPDGS---YGKGPKDACFPIFWVIVFTAFRVIVMD 134
                                    YVLDKI-----NKRMQFTKAKQNKFNESGQFSVFYFFSCIW--GTFILISENCLSDPT 150
                                                                                                           151 LIWKARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKK---QDIPRQLVYIGLHL--- 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Gorley, Neil C.
APPLICANT: Shah, Purvi
APPLICANT: Lal, Preeti
TITLE OF INVENTION: HUMAN LONGEVITY-ASSURANCE PROTEIN HOMOLOGS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/902,853
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Parmaceuticals, Inc. CITY: Palo Alto CTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08902853
Patent No. 5945330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
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LIBRARY: HNT2NOT01
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                                                                                107 KRMQFTKAKQNKFNESGQFSVFYFFSCIWGTFILISENCLSDPTLIWKARP-HSMMTFQM 165
                                                                                                             166 KFFYISQLAYWFHAFPELYFQKTKKQDIPRQLVYIGLHLFHITGAYLL----YLNHL--G 219
                                                                                                                                                                                                    181 WYYMIELSFYWSLLFS--IASDVKRKDFKEQIIH-----HVATIILISFSWFANYIRAG 232
                                                                                                                                                                                                                                                                          233 ILIMALHDSSDYLLESAKMFNYAGWKNTCNNIFIVFAIVFIITRLVILPFWILHCTLVYP 292
                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                          271 -----TVGFHLAGSQNRNPDALTGNVNVLAAKIAVLSSSCTIQAYVTWNLITLWLQ---
                                                                                                                                                                                                                                           220 LLLLVLHYFVELLSHMCGLFYFSDEK--YQKGISLWAIVFILGRLVTLIVSVL-----
                                         70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEEQ for Windows DEMONSTRATION Version 2.0D
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/R21/**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.3%; Score 102; DB 3; Length 687; Best Local Similarity 19.3%; Pred. No. 0.0058; Matches 64; Conservative 42; Mismatches 91; Indels 1
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CIT: Lawrenceville
STATE: NJ
6.0%; Score 116; DB 2; I
20.2%; Pred. No. 5.7e-05;
iive 47; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                 331 ITGKLVED-------ERSDREETESSEGEEAA 355
                                                                                                                                                                                                                                                                                                                                                                                                        322 ---RWVEDSNIQASCMKKKRSRSSKKRTENGVGVETS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Albert, Vivian
TITLE OF INVENTION: Glycine Transporter
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAME: BLOOM, Allen
REGISTRATION NUMBER: 29,135
REFERNCE/DOCKET NUMBER: 314572-109
TELECOMMUNICATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-834-467-2; Sequence 2, Application US/08834467; Patent No. 6008015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMpatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acid
TYPE: amino acid
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
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US-08-834-467-2
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                            Best Local
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271 LLGCLGVSWL-----TATFPY 305
                                                                                     86 YMLVAIIIHATIQEYVLDKINKRM--QFTKAKQNKFNESGQFSVFYFFSCIWGTFILIS- 142
                                                                                                               143 ----ENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKKQDIPRQL 197
                                                                                                                                                                                                                                                                                                                                     252 LWAIVF-------ILGRLVTLIV-----SVLTVGFHLAGSQNRNPD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
    IVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVPAAEEQATGSKSLYYYGVKDLATVFF
                                                                                                                                                                                                                                                                               VYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFYFSDEKYQKGIS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.9%; Score 94.5; DB 4; Length 696;
20.8%; Pred. No. 0.043;
Live 43; Mismatches 103; Indels 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: ISM PC Compatible
COMPUTER: ISM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIETCATION: CURROWN>
ATORNEY/AGENT INFORMATION:
NAMME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 31003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/07757342D
Patent No. 6218509
GENERAL INCORMATION:
APPLICANT: IGARASHI, Masao
MINEGISHI, Takashi
NARANURA, Kazuto
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
                                                                                                                                                                                                             366 YNKFHNNCYRDSVII------SITNCA---
                                                                                                                                                                                                                                                                                                                                                                                                                         286 ALTGNVNVLAAKIAVLSSSCTIQAYVTWNLI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| | | | | | :
---FLLGIPLTSQAGIYWLLL 507
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-07-757-342D-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEFAX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 696 amino acids
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STATE: Massachusetts
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Best Local Similarity 20.8%
Matches 75; Conservative
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                                       271 LIGCLGVSWL-----TATFPY 305
                                                                                86 YMLVAIIIHATIQEYVLDKINKRM--QFTKAKQNKFNESGQFSVFYFFSCIWGTFILIS- 142
                                                                                                                          306 VVLTILFVRGVTLEGAFDGIMYYLTPQWDKILEAKVWGDAASQIFYSLACAWGGLITMAS 365
                                                                                                                                                                 143 ----ENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKKQDIPRQL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                             26 IVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVPAAEEQATGSKSLYYYGVKDLATVFF
                                                                                                                                                                                                                                                                                                                                     ---SVLTVGFHLAGSQNRNPD
                                                                                                                                                                                                                                                     198 VYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFYFSDEKYQKGIS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91; Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FRASESO for Windows DEMONSTRATION Version 2.0D
APPLICATION DATE:
APPLICATION DATE:
APPLICATION NUMBER: US/09/396,177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.3%; Score 102; DB 4; Length 687; Best Local Similarity 19.3%; Pred. No. 0.0058; Matches 64; Conservative 42; Mismatches 91; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Albert, Vivian
TITLE OF INVENTION: Glycine Transporter
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: 997 Lenox Drive, Building 3, Suite 210
CITY: Lavrenceville
                                                                                                                                                                                                         366 YNKFHNNCYRDSVII------SITNCA----
                                                                                                                                                                                                                                                                                                                                     252 LWAIVF-------ILGRLVTLIV----
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APPLICATION NUMBER: 08/834,467
FILING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: BLOOM, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 314572-109
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                      286 ALTGNVNVLAAKIAVLSSSCTIQAYVTWNLI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09396177 Patent No. 6251617 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 687 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
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Gaps

89; Indels 140;

42; Mismatches

Conservative

63;

Matches

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385 ISPLWSLLFFFMLILLGLGTQFCLLETLVTAIVDEVGNEWILQKKTYVTLGVAVAG---- 440
                                                                  -----VVFLCLIRGV------KSSGKVVYF-----TATFPY 256
                                                                                                                86 YMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNES-----GQFSVFYFFSCIWGTFIL 140
                                                                                                                                                          257 VVLTILFVRGVTLEGAFTGI---MYYLTPKWDKILEAKVWGDAASQIFYSLGCAWGGLIT 313
                                                                                                                                                                                                          141 IS-----ENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKKQDIP 194
                                                                                                                                                                                                                                                                                                  195 RQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFYFSDEKYQKGIS--- 251
                                                                                                                                                                                                                                                                                                                                         338 -TSVYAGFVIFSILG---FMANHLGVDV-----SRVADHGPGLAFVA---YPEALTLLP 384
                                                                                                                                                                                                                                                                                                                                                                                             ----SVLTVGFHLAGSQNR 282
                       26 IVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVPAAEEQATGSKSLYYYGVKDLATVFF 85
                                                                                                                                                                                                                                                     314 MASYNKFHNNCYRDSVII------SITNCA------SITNCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A GLYCINE TRANSPORTER AND USES
NUMBER OF SEQUENCES: B
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 638;
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                                                                                                                                                                                                                                                                                                                                                                                             252 ---LWAIVF------ILGRLVTLIV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 NPDALTGNVNVLAAKIAVLSSSCTIQAYVTWNLI 316
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--FLLGIPLTSQAGIYWLLL 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,783B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08240783B
Patent No. 5756348
GENERAL INFORMATION:
APPLICANT: Smith, Kelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRB PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATORNEY REPRESENTION:
ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPRENCE/DOCKEY NUMBER: 1795,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 279-0400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borden, Laurence A.
Branchek, Theresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 638 amino acids
amino acid
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                                                                  222 LLGCLGVSWV----
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US-08-240-783B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-240-783B-2
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                                                                                                                                                                                ----AKQNKFNESGQFSVFYFFSCIWGTFILISENCLSDPTLIWKARPHSMMTFQMKFFY 169
                                                                                                                                                                                                                                                                                                                                                                                               266 IVSV--LTVGFHLAGSQNRNPDALTGNVNVLAAKIAVLSSSCTIQAYVTWNLITLWLQRW 323
                              234 LOALPSYGLESIQTLI------ATSSYSLKKLPSREKFTNLLDATLTYPSHCCAF 282
                                                                                                                                                                                                                           283 RNLPTKEONFS----FSIFKNF-----SKOCES-----TARRPNNETLYSAIFA 322
                                                                                                                                                                                                                                                                           ISQLAYWFHAF------PELY--FQKTKKQDIPRQLVYIGLHLFHITGAYLLY 214
    --EEQATG
                                                                                                                                                                                                                                                                                                                                                                     LNHLGLLLLVLHYFVELLSH------MCGLFYFSDEKYQKGISLWAIVFILGRLVTL
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                                                                                          SKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08295814E
Patent No. 5658786
GENERAL INFORMATION:
APPLICANT: Smith, Kelli E.
APPLICANT: Borden, Laurence A.
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING TAURINE AND GABA
TITLE OF EQUENTION: TRANSPORTERS AND USES THEREOF;
NUMBER OF ESQUENCES: 35
CORRESPONDENCE ADDRESS:
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Pred. No. 0.057;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/295,814E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
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4.8%;
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Best Local Similarity 18.99
Matches 63; Conservative
                                      Conservative
     Query Match
Best Local Similarity
Matches 63; Conserva
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LENGTH: 638
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                    15;
                                                                          222 LIGCLGVSWV------VVFLCLIRGV------KSSGKVVYF----TATFPY 256
                                                                                                                  86 YMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNES-----GQFSVFYFFSCIWGTFIL 140
                                                                                                                                                  257 VVLTILFVRGVTLEGAFTGI---MYYLTPKWDKILEAKVWGDAASQIFYSLGCAWGGLIT 313
                                                                                                                                                                                                                                                   195 RQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFYFSDEKYQKGIS--- 251
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                                                                                                                                                                                                                                                                                  338 -TSVYAGEVIFSILG---FMANHLGVDV-----SRVADHGPGLAFVA---YPEALTLLP 384
0.057;
ches 89; Indels 140; Gaps
                                                  26 IVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVPAAEEQATGSKSLYYYGVKDLATVFF 85
                                                                                                                                                                                                         :: || | :| | 314 MASYNKFHNNCYRDSVII-----SITNCA-----SITNCA----
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APPLICANT: Smith, Kelli
APPLICANT: Borden, Laurence A.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A GLYCINE TRANSPORTER AND USES
TITLE OF INVENTION: BNA ENCODING A GLYCINE TRANSPORTER AND USES
TITLE OF SEQUENCES: 8
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2; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,813
FILING DATE: 26-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09084813 Patent No. 6127131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)391-0525
                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212)391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 18.98;
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amino acid
                 63; Conservative
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CITY: New York
STATE: New York
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 Best Local Similarity
Matches 63; Conser
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TITLE OF INVENTION: DNA Encoding Taurine and GABA Transporters and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 40558-D
CURRENT APPLICATION NUMBER: US/09/343,361
CURRENT PILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN Ver. 2.0 - beta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 -TSVYAGEVIFSILG---FMANHLGVDV-----SRVADHGPGLAFVA---YPEALTLLP 384
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                                                                                                                                        Gaps
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0.057;
ches 89; Indels 140;
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DB 3; Length 638;
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      Score 93; DB 3;
Pred. No. 0.057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.8%; Score 93; DB
18.9%; Pred. No. 0.05
ive 42; Mismatches
                                                                                                                           42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 13, Application US/09343361
; Patent No. 6225115
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441
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                                                                                                                                                                                                                                     APPLICANT: Smith, Kelli
APPLICANT: Borden, Laurence A.
APPLICANT: Barachek, Theresa
APPLICANT: Hartig, Paul R.
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING A GLYCINE TRANSPORTER AND USES THEREOF NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 YMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNES-----GQFSVFYFFSCIWGTFIL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 VVLTILFVRGVTLEGAFTGI --- MYYLTPKWDKILEAKVWGDAASQIFYSLGCAWGGLIT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 IS-----ENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKKQDIP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 RQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFYFSDEKYQKGIS--- 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 -TSVYAGFVIFSILG---FMANHLGVDV-----SRVADHGPGLAFVA---YPEALTLLP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LWAIVF-----SVLTVGFHLAGSQNR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 IVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVPAAEEQATGSKSLYYYGVKDLATVFF 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.8%; Score 93; DB 5; Length 638; 18.9%; Pred. No. 0.057; arive 42; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 MASYNKFHNNCYRDSVII-----SITNCA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 30 ROCKGIELLET FLAZA
CITY: New York
STATE: New YORK
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN RElease #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09662
FILING DATE: 19921112
CLASSIFICATION:
AME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 1795/39875-A-PCT
TELEPOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9809
TELERX: (212) 977-9809
TELERX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEDURANE: CRRACATERISTICS:
FUNDAME.
283 NPDALTGNVNVLAAKIAVLSSSCTIQAYVTWNLI 316
                                                     ---FLLGIPLTSQAGIYWLLL 458
                                                                                                                                                                                     Sequence 2, Application PC/TUS9209662 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 638 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein PCT-US92-09662-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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33 FFLLGLVFEGTAEASIVFLTLQHSVAVP-----AAEEQATGSKSLYYYGVKDLATVFFYM 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45; Indels
                                                                                                                                             Sequence 6, Application US/08336031
Patent No. 5817782
GENERAL INFORMATION:
APPLICANT: Jazwinski, S. M.
TITLE OF INVENTION: LAG1: A GENE FOR INCREASING THE
TITLE OF INVENTION: LONGEVITY OF EUKARYOTES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 LVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNESGQFSVFY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/336,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 86; DB 2;
Pred. No. 0.062;
                                                                                                                                                                                                                                                                                                                               E: Scully, Scott, Murphy & Presser 400 Garden City Plaza
283 NPDALTGNVNVLAAKIAVLSSSCTIQAYVTWNLI 316
                                         ---FLLGIPLTSQAGIYWLLL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6, 2002, 17:10:39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,875
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
AMAME: DIGIGILO, Frank
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 93
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SAS UR
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.5%;
Best Local Similarity 26.5%;
Matches 27; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 193 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                     United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-336-031-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: September
Job time: 7973 sec
                                                                                                                                                                                                                                                                                                                                                   STREET: 400 Garden
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: Un
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

6, 2002, 17:11:51 ; Search time 52.02 Seconds
(without alignments)
681.603 Million cell updates/sec September Run on:

US-09-807-470-4 1920 1 MGLRKKSTKNPPVLSQEFIL.....VGVETSNRVDCPPKRKEKSS 369 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	translocating chai	translocating chai				longevity-assuranc	hypothetical prote	longevity assuranc	NADH dehydrogenase	hypothetical prote	probable transport	hypothetical prote	NADH dehydrogenase	hypothetical prote	hypothetical 52.9	hypothetical prote	glycine transporte	glycine transporte	dipeptide transpor	Na+/H+ antiporter	hypothetical prote	probable integral	probable membrane	hypothetical prote	ubiquinol cytochr	cytochrome-c oxida	hypothetical prote	iron (III) ABC tra	ABC transporter (a
SUMMARIES	ΙĐ	S21736	S30034	T19417	T19419	S46800	T38012	S30134	T40389	B84949	T27324	AG1051	T20916	T11411	A86116	D65230	A98275	177912	157956	AE3306	A69845	F97765	AB1260	S64153	н86268	S07743	S21042	S07749	D64048	D70048
	DB	~	7	~	~	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	~	7	7	7	~	7	7	7	7
	Length	374	374	371	373	411	390	418	357	614	360	476	331	459	484	484	484	638	. 692	347	614	207	740	802	308	391	517	387	206	469
æ	Query	73.2	72.5	25.7	25.4	7.5	6.7	6.4	6.1	0.9	8	5.7	5.5	5.5	5.5	5.5	5.5	5.3												5.0
	Score	1405.5	1392.5	494	487	144	128	123.5	116.5	115	111.5	108.5	106.5	106.5	106.5	105.5	105.5	102	102	101	100.5	99.2	66	66	98.5	98.5	98.5	86	97.5	96.5
	Result No.	1	7	m	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	hypothetical prote	hypothetical prote	virulence factor M	hypothetical 53.7	probable transport	probable transport	lutropin-choriogon	hypothetical prote	amino acid transpo	hypothetical prote	NADH dehydrogenase	ABC transporter (p	glycine transporte	glycine transport
T48586 B96642	T15177	T27121	H70453	C65147	H91174	н86020	A41344	D83913	66003	T38922	S78183	B84139	158140	JH0673
2.0	7	~	7	7	~	~	~	7	7	7	~	~	7	7
1123	835	1564	499	489	489	489	969	214	512	394	493	648	633	638
0.0	5.0	5.0	6.4	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.8	4.8
96	95.5	95.5	95	94.5	94.5	94.5	94.5	94	94	93.5	93.5	93.5	93	66
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 \$21736 translocating chain-associating membrane protein - dog C; Species: Canis lupus familiaris (dog) C; Species: Canis lupus familiaris (dog) C; Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 24-Sep-1999 C; Accession: \$21736 C; Accession: \$21736 Nature 357, 47-52, 1992 A; Title: A protein of the endoplasmic reticulum involved early in polypeptide transle A; Reference number: \$21736; MUID:92244357 A; Status: preliminary A; Mccession: \$21736 A; Status: preliminary A; Mcloss in Protein CfCS A; Status: Dressidues: 1-74 <gos> A; Cross-references: EMBL:X63678; NID:9941; PIDN:CAA45217.1; PID:9942 C; Superfamily: translocating chain-associating membrane protein C; Keywords: transmembrane protein</gos>	ry Ma t Loc ches 1 1	121 ESGQFSVFTESCINGTFILLSENCISPATITHATIQUIVENTURANGEN	181 PELYFOKTKKEDIPRQLVYIGLYLFHIAGAYLLNLHHLGLVLLVLHYEVEFLFHISRLFY 240 241 FSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAKIAV 300
RESULT S21736 transl C; Spec C; Date R; Goer Nature A; Refe A; Refe A; Stat A; Mole A; Resi A; Resi A; Resi A; Resi C; Supe C; Supe	Que Bes Mat Qy Db	· 3	

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A;Cross-references: EMBL:AL022716; PIDN:CAA18772.1; GSPDB:GN00022; CESP:C24F3.1b
A;Experimental source: clone C24F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T19419
R;McMurray, A.
                                                                                                                                                                                                                                                                                                                                                            118 KFNESGQFSVFYFFSCIWGTFILISENCLSD-----PTLIWKARP--HSMMTFQMKFFYI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 AVEQGOEREVHG---YLSGILDLPAIFFYSVCWIVVHAVVQEYGLDKISKKTHLSKVSTF 123
                                                                                                                                                                                                                                                                      KFNESGQFSVFYFFSCIWGTFILISENC -- LSDPTLIWKARP -- HSMMTFQMKFFYISQL 173
                                              Gaps
                                                                                                                                                                                58 AVPAAEEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 AVPAAEEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQN 117
                                                                                                               HMCGLFYFSDEKYQKGIS-----LWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : ||:|| ||:|| ||:|| ||:|| ||:||:| | ::|
7 GSKASKKPQPPILSHEFIIQNHGDIMSCVVWVFIVGLMFPLTHSLSSLFIAPQYNGTYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNVNVLAAKIAVLSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKKRS-----RS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GLRKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQ----HSV
                                                                                        2 GLRKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQ----HSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
                                            30;
  Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 114/3; 158/2; 365/3
C;Superfamily: translocating chain-associating membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.4%; Score 487; DB 2; Length 37 32.4%; Pred. No. 5.2e-35; Live 73; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C24F3.1b - Caenorhabditis elegans
25.7%; Score 494; DB 2;
llarity 32.4%; Pred. No. 1.3e-35;
Conservative 74; Mismatches 144,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, April 1998
A;Reference number: 219122
A;Accession: T19419
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-373 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 32.4%
Matches 120; Conservative
                       Local Similarity
nes 119; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 SKKRTEN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 ::
357 EKKRQDS 363
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    Query Match
                       Best Loca
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                                                                                                        C; Accession: S30034
R; Goarlich, D.; Hartmann, E.; Prehn, S.; Rapoport, T.A.
Nature 357, 47-52, 1992
A; Title: A protein of the endoplasmic reticulum involved early in polypeptide translocat A; Reference number: S21736; MUID: 92244357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:CAA18770.1; GSPDB:GN00022; CESP:C24F3.1a
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T19417
                                                                   Species: Homo sapiens (man)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESGQFSVFYFFSCIWGTFILISENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAEEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKK----RSRSSKKRTENGV-GVETS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGLRKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                    A;Molecule type: mRNÅ
Ksesidues: 1-374 <GOED-
A;Cross-references: EMBL:X63679; NID:937264; PIDN:CAA45218.1; PID:937265
C;Superfamily: translocating chain-associating membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAKIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PELYFQKTKKQDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 4
A;Introns: 114/3; 158/2; 363/3
C;Superfamily: translocating chain-associating membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                            chain-associating membrane protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C24F3.1a - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 72.5%; Score 1392.5; DB 2 Best Local Similarity 71.4%; Pred. No. 2.2e-114; Matches 267; Conservative 44; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-371 <WIL>
A;Cross-references: EMBL:AL022716; PIDN:CAA18770.1;
A;Experimental source: clone C24F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;McMurray, A.
submitted to the EMBL Data Library, April 1998
A;Reference number: 219122
A;Accession: T19417
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NVADSPRNKKEKSS 374
                                                                                                                                                                                                                                                 A; Status: preliminary
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C; Genetics:

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A.Wolecule type: DNA
A.Residues: 1-418 <BOY>
A.Residues: 1-418 <BOX>
A.Crossreferences: GB.S59773; NID:g300231; PIDN:AAC60549.1; PID:g300232
A.Crossreferences: GB.S59773; NID:g300231; PIDN:AAC60549.1; PID:g300232
A.Crossreferences: Strain S288C
R.Boyer, J.; Pascolo, S.; Richard, G.F.; Ghazvini, M.; Colleaux, L.; Thierry, A.; Mol. Submitted to the Protein Sequence Database, March 1994
A.Recression: S37813
A.Accession: S37819
A.Molecule type: DNA
A.Residues: 1-418 <BO2>
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                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:299258; PIDN:CAB16359.1; GSPDB:GN00066; SPDB:SPAC1A6.09c
A;Experimental source: strain 972h-; cosmid c1A6
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein YKL008c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YKL156
C;Species: Saccharomyces cerevisiae
C;Date: 18-Jun-1993 #sequence_revision
C;Accession: S30134; S37819; S17017
R;Boyer, J; Pascolo, S; Richard, G.F.; Dujon, B.
Yeast 9, 279-287, 1993
A;Title: Sequence of a 7.8 kb segment on the left arm of yeast chromosome XI 3
                                                                                    longevity-assurance protein 1 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T38012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVLDKI-----NKRMQFTKAKQNKFNESGQFSVFYFFSCIW--GTFILISENCLSDPT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---FHITGAYLLYLNHLGLLLL----VLHY--FVELLSHMCGLFYFSDEKYQKGISLWAI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 V--FILGRLVTLIVS---VLTVGFHLAGSQNRNPDALTGNVNVLAAKIAVLSSSCTIQAY 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRHYLFSKILRVVVTNAPEIIGGFHL------DVPNGYIFNKPIYIAFILLLFTLQL- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 SIVFLTLQHSVAVPAAE-----EQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 GFNFLRVGNAILYIFDLSDYILSGGKMLKYLGFGKICDYLFGIF------VASWVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIWKARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKK---QDIPRQLVYIGLHL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yeast (Saccharomyces cerevisiae)
protein YKL156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 128; DB 2; Le
Pred. No. 0.0016;
52; Mismatches 119;
                                                                                                                                                                C, Accession: T38012

By Churcher, C.M.

submitted to the EMBL Data Library, September 1997

A; Reference number: 221761

A; Accession: T38012

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Residues: 1-390 <CHU>
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A;Reference number: S30132; MUID:93255906
A;Accession: S30134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Gene: lag1; SPDB:SPACIA6.09c
A; Map position: 1
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Best Local Similarity 22.0
Matches 68; Conservative
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» Jobsoription: The sequence of S. cerevisiae cosmid 9780.

» Reference number: $46797

» Accession: $46800

» Minolecule type: DNA

» Residuaes: 1-411 cFAV>

» Residuaes: 1-411 cFAV>

» Accession: $6800 A. M.; Franklin, D.S.; Kale, S.P.; Pinswasdi, C.; Jazwinski, J. Biol. Chem. 269, 15451-15459, 1994

» Title: Cloning and characterization of LAG1, a longevity-assurance gene in yeast.

» Reference number: A54012; MUID:94253121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-172,'IV',175-219,'C',221-300,'TEISGI',314,'EKQE',315,'DSNDNPTE',324,'A',32','A',32','A',32','A',32','A',38','ACQB',386,'L',388,'NRLARNNEK' <DAM>A;Cross-references: GB:U08133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAGI protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YHL003c
C;Species: Saccharomyces cerevisiae
C;Species: 28-oct.1994 #sequence_revision 28-oct-1994 #text_change 23-Mar-2001
C;Accession: S46800; A54012
                                                                                                                                                                                               88 LVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNESGQFSVFYF-FSCIWGTFILI-SENC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 IFFTFLREFLMDVVIRPFTVYLNVTSEHRQKRMLEQMYAIFYCGVSGPFGLYIMYHSDLW 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEKTKPMYRTYPVITNPFLFKIFYLGQAAFWAQQACVLVLQLEKPRKDYKELVFHHIVTL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :|: :|| : 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 FFLLGLVFEGTAEASIVFLTLQHSVAVP----AAEEQATGSKSLYYYGVKDLATVFFYM 87
182 FQISYWIHQFPEFYLQKLKRDEIRQKSVQAILHIAFISIAYFFNFTRVGLALITLEYITQ
                                                        LLSHMCGLFYFSDEKYQKGIS-----LWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPD
                                                                                    FHITGAYLLYLNHLGLLLLV-------LHYFVELLS-HMCGLFY-----
                                                                                                                                                                286 ALTGNVNVLAAKIAVLSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKKRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.5%; Score 144; DB 2; Length 411; 22.6%; Pred. No. 6.8e-05; Live 49; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FSDEKYQKGISLWAIVFILGRLVTLI 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: involved in dertermination of longevity C; Superfamily: hypothetical protein YKL008c C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: SGD:LAG1
A;Cross-references: SGD:S0000995; MIPS:YHL003c
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                                                                                                                                                                                                                                                                        340 -RSSKKRTEN 348
                                                                                                                                                                                                                                                                                                         : | | | : 356 PKKEKKRQDS 365
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Best Local Similarity
Matches 65; Conserv
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C; Function:
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Length 357;

; Score 116.5; DB 2; ; Pred. No. 0.015; 41; Mismatches 121;

61

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57 VAVPAAEEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQF-TKAK 115
                                                                                              2 GLRKKSTKNPPVLSQEFILQNHAD -- IVSCVGMFFLLGLVF--- EGTAEASIVFLTLQHS 56
                                                                                                                             7 GRRRRSKSIVGRAAQNAVLRSKEKTWIVPLILLTLIVGWYFVNPNGYIKYGI-FL----S
                    6.1%;
                                                           Conservative
                                         Similarity
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163 NNLCAF-----
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Best Local Simi
Matches 59;
                    Query Match
                                           Local
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                                                         Matches
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A;Cross-references: EMBL:Z28008; NID:9485982; PIDN:CAA81843.1; PID:9485983; MIPS:YKL008d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              longevity assurance protein homolog SPBC3E7.15c - fission yeast (Schizosaccharomyces C:Species: Schizosaccharomyces pombe C:Species: 03-Dec-1999 **sequence_revision 03-Dec-1999 **text_change 31.Jan-2000 C:Accession: T40389; T40499 R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Brown, D.; Churcher, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Residues: 1-357 CLYN>
A:Cross-references: EMBL:AL023534; PIDN:CAA19018.1; GSPDB:GN00067; SPDB:SPBC3E7.15c
A:Experimental source: strain 972h-; cosmid 63E7
R:GWilliam, R.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
A:Reference number: 221933
A:Reference number: 221933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-357 <GWI>
Cross-references: EMBL:AL031534; PIDN:CAA20722.1; GSPDB:GN00067; SPDB:SPBC4F6.02c
Experimental source: strain 972h-; cosmid c4F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, May 1998
A:Reference number: Z21924
A:Reference number: Z21924
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Resolute: preliminary; translated from GB/EMBL/DDBJ
A:Residner. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 EATKNDSDLVKKIWFSFREISYRHAWIAPLMILIAVYSAYFTSG----NTTKTNVLHRFV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLQHSVAVPAAEEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLLLLV-----LHYFVELLSHM-CGLFYFSDEKYQKGISLWAIVFILGR---LVTLIV 267
                                                                                                                                                                                                                                                                                                                                                                                                 6 KSTKNPPVLSQEF-----ILQNHADI-----VSCVGMFFLLGLVFEGTAEASIV--FL 51
                                Rymatruda, J.F.; Gattermeier, D.G.; Cooper, J.A.
submitted to the EMBL Data Library, August 1991
A; Description: Yeast capping protein.
A; Reference number: S17016
A; Accession: S17017
A; Accession: S17017
A; Accession: S17017
A; Residues: 1-149 < AMA>
A; Cross-references: EMBL:X61398; NID:g455515; PIDN:CAA43670.1; PID:g3445
C; Genetics:
A; Map position: 11L
C; Superfamily: hypothetical protein YKL008C
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---FFNTKAMYRTYPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 MMTFQMKFFYISQLAYWFHAFPELYFQKTKKQDIPRQLVYIGL-HLFHITGAYLLYLNHL
                                                                                                                                                                                                                                                                                                                     Length 418;
                                                                                                                                                                                                                                                                                                                   6.4%; Score 123.5; DB 2;
19.4%; Pred. No. 0.0043;
tive 59; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 TSKHRIKRIMEQMYAIFYTGVSGPFGIYCMYHSDLW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: SPBC3E7.15c; SPBC4F6.02c
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 19.49
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||||
SVLT 331
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C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C; Accession: B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B49494 B4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Buchnera sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196
                                                                                      116 LRRFEEQAYTCLYFTVMGSWGLYVMKQTPMWFFNTDAFWEEXPHFYHVGSFKAFYLIEAA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 YGVSILKNNNQVF-TQILWKWL--SINEFKIDFGFFLDGLSLSMLFVITGVGLLIHIFSS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 LYFOKTKKQDIPRQLVYIGLHLFHITGAYL----LYLNHLGL----LLLVLHYFVELL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 SHMCGLFYFSDEKYQKGISLWAIVFILGRL--VTLIVSVLTVGFHLAGSQNRNPDALTGN 290
116 QNKFNESGQFSVFYFFSCIWGTFIL-ISENCLSDPTLIWKARPHSMMTFQMKFFYISQLA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 WGTFILISENCLSDPTLIWKARPHSMMTFQMKF------FYISQLAYWFHAFPE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 LATVFF---YMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNESGQFSVF--YFFSCI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSIIFFIILFPLIGFLFLSTIQDFIFKRYTLNI------GIFSIFISFFITCF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90;
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                                                                                                                                                                                                                                                                                                             NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain L [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91; Indels
                                                                                                                                                                                                                                                YWFHAFPELYFOKTK-KODIPROLVYIGLHLFHITGAYLLYLNHLGLLLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: nuoL; BU164
C;Superfamily: NADH dehydrogenase (ubiquinone) chain
C;Keywords: NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 115; DB 2, Pred. No. 0.037; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSPDB: GN00144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 20.2%; Pre
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A;Experimental source: strain APS
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us-09-807-470-4.rpr

Sat

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T11411
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - cat mitochondrion (fragment) (S.) species: mitochondrion Felis silvestris catus (domestic cat)
C.) Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 12-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aypothetical protein F14F8.3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Accession: T20916
R.Lloyd, C.
Submitted to the EMBL Data Library, March 1997
A.Reference number: 219346
A.Accession: T20916
A.Accession: T20916
A.Accession: T20916
A.Accession: T20916
A.Accession: T20916
A.Accession: EMBL.Z92782; PIDN:CAB07188.1; GSPDB:GN00023; CESP:F14F8.3
A.Cross-references: EMBL.Z92782; PIDN:CAB07188.1; GSPDB:GN00023; CESP:F14F8.3
A.Experimental source: clone F14F8
A.Gene: CESP:F14F8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 FILTHLGLLILDWANYQGSLSQIPTLYYL------CYFIFLNIIQITSAILYI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---VFFYMLVAIIIHATIQEYVLDKINK 107
                                                                                          -- ISENCLSDPTLIWKA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 SKSLYYYGVKDLA-----TVFFYMLVAIIIHATIQEYVLDKINKRMQFTKA--- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----WGTFILISENCLSDPTLIWKARP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSMMTFQM---KFFYISQLAYWFHAFPEL--YFQKTKKQDIPRQLVYIGLHLFHITGAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYLNHLGLLLLVLHYFVELLSHMCGLFYFSDEKYQKGISLWAIVFILGRLVTLIVSVLTV
                                                                                                                                                                                                                                                                    LLYLNHLGLLLLVLHYFVELLSHMCGLFYFSDEKYQKGISLWAIVFILGRLVTLIVSVLT
                                                                                                                                                                                 RPHSMMTFQMKFF--YISQLAYWFHAFPELYFQKTKKQDIPRQLVYIGLHLFH--ITGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 5
A;Introns: 55/3; 95/2; 242/3; 260/3
C;Superfamily: Caenorhabditis elegans hypothetical protein K02H11.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                          RMQFTKAKQNKFNESGQFSV-FYFFS-CIWGTFIL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.5%; Score 106.5; L
24.2%; Pred. No. 0.1;
:ive 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                            272 VGFHLAGSQNRNPDALTGNVNVLAAKIAVLSS 303
                                                                                                                                                                                                                                                                                                                                                                                                      EAFN-GISORLIPGA-----VLAIDCAAIYS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 KONKFNESGQFSVFYFFS--CI-----
    67 TGSKSLYYGVKD-----LAT-
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Matches 63; Conserv
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R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy A; Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable transport protein SgaT sgaT [imported] - Salmonella enterica subsp. enterica (S.Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi (C.Species has also been called Salmonella typhi (C.Spate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                submitted to the EMBL Data Library, October 1998
A;Reference number: 220345
A;Reference number: 220345
A;Reference number: 220345
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: DNA
A;Residues: 1-360 <WILL>
A;Cross-references: EMBL;AL03255; PIDN:CAA21723.1; GSPDB:GN00019; CESP:Y6B3B.10
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-476 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06860.1; PID:g16505508; GSPDB:GN00176
C;Genetics:
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 KKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVPA--- 61
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                                                                                                                                                                                                                                                                                                                                                                                                                             55;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                 Score 111.5; DB 2;
Pred. No. 0.041;
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                                                                                                                                                                                                                                                                                                                                                                                                                          55; Mismatches
                                                                                                                                                                                                                                                                                         A; Map position: 1
A; Introns: 24/3; 58/1; 88/3; 143/1; 205/2; 310/3
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                                                                                                                                                                                                                           A; Experimental source: clone Y6B3B
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A;Gene: CESP:Y6B3B.10
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Best Local Simi
Matches 73;
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Best Local S
Matches 57,
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211
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                                                                  RPHSMMTFQMKFF--YISQLAYWFHAFPELYFQKTKKQDIPRQLVYIGLHLFH--ITGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 484;
146 IRTIMLTGHIMFQQAGLIAVTLFIFGYSMWTTIICTAILVSLYWGITSNMMYKPT
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                                                                                                                                                                                                                                                                                 272 VGFHLAGSQNRNPDALTGNVNVLAAKIAVLSS 303
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nes 72; Conserv
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Best Local S:
Matches 72;
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-484 <STO>
A;Cross-references: GB:AE005174; NID:g12519184; PIDN:AAG59389.1; GSPDB:GN00145; UWGP:Z58
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein sgaT [imported] - Escherichia coli (strain O157:H7, substrain EDL93 (S. Species: Escherichia coli (S. Species: Escherichia coli (C. Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 (S. Accession: A86116)
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Nature 409, 529-533, 2001
A. Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A. Reference number: A88480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                A;Note: ND4
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
         Eliopez, J.V.; Cevario, S.; O'Brien, S.J.
Genomics 33, 229-246, 1996
Genomics 33, 229-246, 1996
A.Title: Complete nucleotide sequences of the domestic cat (Felis catus) mitochondrial
A.Fitle: Complete nucleotide sequences of the domestic cat (Felis catus) mitochondrial
A.Fitle: Complete nucleotide MUD:96301400
A.Accession: Til411
A.Scatus: preliminary; translated from GB/EMBL/DDBJ
A.Gelcule type: DNA
A.Residues: 1-459 CLOP>
A.Cross-references: EMBL:U20753; NID:g1098523; PID:g1098533; PIDN:AAC48578.1
A.Scatus: mitochondrion
A.Genome: mitochondrion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RMQFTKAKQNKFNESGQFSV--FYFFSCIWGTFIL-----ISENCLSDPTLIWKA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 TFILISENCLSDPTLIW-KARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKKQD--- 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----FSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDAL 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 TAMLMPMTCLSKPNMIWINSTTYSLLISLISLSYLNQLGGHSLNFSLLFFSDSLSAPLLV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 TGNVNVLAAKIAVLSSSCTIQAYVTWNLITLW--------LORWVEDSNIQA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 NPPVLSQEFILQNHADIVSCVGMFFL---LGLVFEGTAEASIVFLTLQHSVAVPAAEEQA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 NAPLL------LGIVTCLGYILLRKSVSVIIKGTIKTIIGFMLLQAGSGILTSTFKP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 67;
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          82;
                                                                                                                                                                                                                                                                                                                                                                                                             / Match 5.5%; Score 106.5; DE Local Similarity 21.3%; Pred. No. 0.15; nes 51; Conservative 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Search completed: September 6, 2002, 17:11:52 Job time: 6791 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 6, 2002, 17:21:14; Search time 26.42 Seconds (without alignments) 540.784 Million cell updates/sec Run on:

US-09-807-470-4
1920
1 MGLRKKSTKNPPVLSQEFIL.....VGVETSNRVDCPPKRKEKSS 369 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

105224 Total number of hits satisfying chosen parameters: 105224 seqs, 38719550 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	iption	can	homo s	bos t	Q15035 homo sapien		P78970 schizosacch	P28496 saccharomyc	059735 schizosacch	puchne	felis sil	P39301 escherichia	P48067 homo sapien				-					P16582 sus scrofa	Q10260 schizosacch		Q28585 ovis aries	Q28039 bos taurus	010487 schizosacch		Q50361 mycoplasma	P28571 mus musculu	Q04690 mus musculu	P40441 saccharomyc	Q9pr97 ureaplasma	P52166 caenorhabdi
SUMMARIES	DI	TR	TRAM_HUMAN	TRAM_BOVIN	Y557_HUMAN	LAG1_YEAST	LAG1_SCHPO	YKA8_YEAST	YHXF_SCHPO	NUOL_BUCAI	NU4M_FELCA	SGAT_ECOLI	S6A9_HUMAN	YGN9_YEAST	CYB_PARTE	HITB_HAEIN	QOX1_SULAC	YM14_PARTE	CYB_TOXGO	MVIN_AQUAE	YHIP_ECOLI	LSHR_PIG	YD2C_SCHPO	S6A9_RAT	LSHR_SHEEP	S6A9_BOVIN	YDFG_SCHPO	PDRA_YEAST	Y316_MYCPN	S6A9_MOUSE	NF1_MOUSE	YIRO_YEAST	Y048_UREPA	SE12_CAEEL
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	Score	0	1387.5	1331.5	832.5	144	128	123.5	116.5	115	106.5	105.5	102	66	98.5	98.5	98.5	86	95.5	95	94.5	94.5	93.5	93	92.2	91	90.5	06	88	68	88	88.5	88.5	88
	Result No.	1	7	m	4	S	9	7	œ ·	on ;	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q22549 caenorhabdi Q20076 caenorhabdi	P75134 mycoplasma O67472 aquifex aeo P40886 saccharomyc	Q04182 saccharomyc P75463 mycoplasma O84068 chlamydia t	Q9hcx4 homo sapien P97526 rattus norv	P21359 homo sapien P81318 methanococc
AEEL AEEL	YCPN QUAE EAST	EAST YCPN HLTR	UMAN T	man Etja
INXA_C	Y443_MYCPN YF02_AQUAE HXT8_YEAST	PDRF_Y Y225_M TLC1_C	TRP7_H	NF1_HUMAN YC8A_METJP
559 836	401 388 569	1529 491 528	862 2820	2839 254
<b>4</b> .6	4 4 4 6 5 5 5	4 4 4 v.v.v.	4.4	4.5
88 88	87.5 87 87	86.5 86.5 86.5	86.5 86	85.5
34 35	36 37 38	39 40 41	4 4 3	44 45

### ALIGNMENTS

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Q9GKZ4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE-92244357; PubMed-1315422;
Goerlich D., Hartmann E., Prehn S., Rapoport T.A.;
"A protein of the endoplasmic reticulum involved early in polypeptide
                                                                                                                                                                                                      242
                                                                                                                                                          GQFSVFYFFSCIWGTFILISENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPE 182
                                                                                                                                                                                                                                                  DEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAKIAVLS 302
                                                                                                             EEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNES 122
                                                                                                                         241
                                                                                                                                                                                                                                                                                              SSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKK----RSRSSKKRTENGV-GVETSNR 357
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                       61
                                                                3 LRRKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVPAA 62
                                                                                                                                                                                                                 IRKKSTKSPPVLSHEFILQNHADIVSCVAMVFLLGLMFEITAKASIIFVTLQYNVTLPAT
                                                                                                                                                                                                      LYFOKTKKODIPROLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFYFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Buteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TRAM protein (Translocating chain-associating membrane protein)
                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                     Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STIMULATORY OR REQUIRED FOR THE TRANSLOCATION
SECRETORY PROTEINS ACROSS THE ER MEMBRANE.
-!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.
-!- SIMILARITY: BELONGS TO THE LASSI FAMILY.
                                           Indels
                     DB 1;
                    Score 1400.5; DB Pred. No. 7.5e-108
                                                                                                                                                                                                                                                                                                                                                                                                                      373 AA.
                                           40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                     72.9%;
72.6%;
                               Best_Local Similarity 72.69
Matches 270; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 357:47-52(1992).
                                                                                                                                                                                                                                                                                                                                                        | | | ||||||
362 ADSPRNRKEKSS 373
                                                                                                                                                                                                                                                                                                                                           358 VDCPPKRKEKSS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translocation.
                                          Matches 270;
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                     Query Match
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria: Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 IRKKSTKSPPVLSHEFVLQNHADIVSCVAMVFLLGLMFEITAKASIIFVTLQYNVTLPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 EEQATESVSLYYYGIKDLATVFFYMLVAIIIHAVIQEYMLDKINRRMHFSKTKHSKFNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 NEXYQKGFSLWAVLFVLGRLITLILSVLTVGFGLARAENQKLDFSTGNFNVLAVRIAVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 LYFQKTKKQDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFYFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 DEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAKIAVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKK----RSRSSKKRTENGV-GVETSNR
                                               Transmembrane; Glycoprotein; Translocation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LRKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVPAA
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                                                                                                                                                                                                                                                                                                                                                                      (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Indels
                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (P) C220949AF4EFEDDO CRC64;
                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
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                                                                                                                                 POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                               BY SIMILARITY.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1387.5; DB 1;
; Pred. No. 8.8e-107;
44; Mismatches 57;
                                                                                                                                                                               LUMENAL (POTENTIAL). POTENTIAL.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
TRAM protein (Translocating chain-associating
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71.5%;
53679; CAA45218.1; -. 2000687; AAH00687.1;
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Best Local Similarity 71.59
Watches 266; Conservative
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                                                 Endoplasmic reticulum;
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362 ADSPRNKKEKSS 373
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Tracey
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Matches
          Y557_HUMAN
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                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 VKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNESGQFSVFYFFSCIWG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFYFSDEKYOKGISLWAIV 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFILISENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKKQDIPRQ 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAKIAVLSSSCTIQAYVTWNLI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVPAAEEQATGSKSLYYYG 76
                                                                                                                                                                                                     Transmembrane; Glycoprotein; Translocation
                          Clark T.G., Morris J., Akamatsu M., McGraw R.A., Ivarie R.D.; "Cloning and sequence analysis of a bovine tram cDNA."; Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STIMULATORY OR REQUIRED FOR THE TRANSLOCATION OF SECRETORY PROTEINS ACROSS THE ER MEMBRANE (By similarity).
-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM MEMBRANE (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                         (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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LUMENAL (POTENTIAL).
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LUMENAL (POTENTIAL).
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                                                                                    similarity).
-!- SIMILARITY: BELONGS TO THE LASS1 FAMILY.
                                                                                                                                                                                                                                                                                                             POTENTIAL.
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Best Local Similarity
Matches 257; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                358 AA;
NCBI_TaxID=9913;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
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MEDLINE-96051398; PubMed-7584044;

Nomura N., Magase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,

Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.;

Prediction of the coding sequences of unidentified human genes.

The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced hanalysis of cDNA clones from human cell line KG-1.";

DNA Res. 1:223-229(1994).
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                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE LASSI FAMILY.
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45.1%; Pred. No. 3.1e-61;
tive 72; Mismatches 115;
                                                                                                                          (Rel. 40, Last sequence update)
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                                                 352
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  236 FADENNEKLFSAWAAVFGVTRLFILTLAVLAIGFGLARMENQAFDPEKGNFNTLFCRLCV 295
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
MEDLINE-94378003; PubMed-8091229;
MEDLINE-94378003; PubMed-8091229;
MEDLINE-94378003; PubMed-8091229;
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                   "Cloning and characterization of LAG1, a longevity-assurance gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                         LSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKKR-----SRSSKKRT---ENG
                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO THE LASSI FAMILY.
                                                                                                                                                                                                                      Longevity-assurance protein 1 (Longevity assurance factor 1).
                                                                                                                                                                                                                                                                                                                   STRAIN-X2180-1A;
MEDLINE-9423121; PubMed-8195187;
D'Mello N-V. Childress A.M., Franklin D.S., Kale S.P.,
Pinswasdi C., Jazwinski S.M.;
                                                                                                                                                                                                (Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                           411 AA.
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                                                                        VGVETSNRVDCPPKRKEKS 368
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S0000995; LAG1
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                                                                                                                                                                                                                                  LAGI OR YHL003C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane.
                                                                                                                                                                                   01-FEB-1995
                                                                                                                                                                                                           16-OCT-2001
                                                                                                                                                           LAG1_YEAST
P38703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaudin M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                    IWGGIQKDERSDSDSDESAENEESKEKCE -> TEISGIWE
KQEIDSNDNPTERALSPNETSKQVKPDLLVVLNPTENRNAL
LEAIKSRVPTIAIIDTDSEPSLVTYPIPGNDDSLRSVNFLL
                             F -> C (IN REF. 2).
VFTPFVFGLEVFFMIYLRHVVNIRILMSVLTEFRHEGNYVL
NFATQQYKCWISLPIVFVLIAALQLVNLYWLFLILRILYRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 LVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNESGQFSVFYF-FSCIWGTFILI-SENC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLIWSSYVFHFTKMGLAIYITMDVSDFFLSLSKTLNYLNSVFTPFVFGLFVFFWIYLRHV 320
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 FFLLGLVFEGTAEASIVFLTLQHSVAVP----AAEEQATGSKSLYYYGVKDLATVFFYM 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V., Wood V.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: INVOLVED IN THE AGING PROCESS (BY SIMILARITY).
-! SUBCELLULAR LOCATION: INTEGRAL membrane protein (Potential).
-! SIMILARITY: BELONGS TO THE LASSI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 LSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKKQDIPRQLVYIGL-HL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 LFKTKPMYRTYPVITNPFLFKIFYLGQAAFWAQQACVLVLQLEKPRKDYKELVFHHIVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 FHITGAYLLYLNHLGLLLLV-------LHYFVELLS-HMCGLFY-----
                                                                                                                                                                                                                    GVLARAGORGLONRLARNNEK (IN REF. 1). 91676D56AC053F3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    62;
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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-ON SPACIAGO (Prission peast)
17-ON SCHIZOSACCHARONYCES pombe (Fission peast)
                                                                                                                                                                                                                                                                                                                                                     Score 144; DB 1; Length 411; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----FSDEKYQKGISLWAIVFILGRLVTLI 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 VNIRILWSVLTEFRHEGNYVLNFATQQYKCWISL-PIVFVLIAALQLV 367
                                                                                                                                                                                                                                                                                                                                                                                                                    49; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chanda E.R., Lingner C., Ko Z., Young P.G.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
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Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                     7.58;
                                                                                                                                                                                                                                                                                                                                                                                22.68;
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411
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P78970; 013860;
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                                                                                                          EMBL; X61398; CAA43670.1; -. EMBL; S59773; AAC60549.1; -.
                                                                                                                                    Z28008; CAA81843.1;
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                                                                                                                                                                                 102
155
193
280
317
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SGD; S0001491; YKL008C.
                                                                                                                                                                          protein;
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Best Local Similarity
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                                                                                                                                                                        Hypothetical
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059735;
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YHXF_SCHPO
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Amatruda J.F., Gattermeir D.J., Karpova T.S., Cooper J.A.;
"Effects of null mutations and overexpression of capping protein on morphogenesis, actin distribution and polarized secretion in yeast.";
J. Cell Biol. 119:1151-1162(1992).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE LASS1 FAMILY.
                                                                                                                                                                                                                                                                                                                        247 GFNFLRVGNAILYIFDLSDXILSGGKMLKYLGFGKICDYLFGIF------VASWYY 296
                                                                                                                                                                                                                                                           100 YVLDKI------NKRMQFTKAKQNKFNESGQFSVFYFFSCIW--GTFILLSENCLSDPT 150
                                                                                                                                                                                                                                                                                   135 YVFRPFVLNWGVRNRKVII-----RFCEQG-YSFFYYL-CFWFLGLYIYRSSNYWSNEE 186
                                                                                                                                                                                                                                                                                                                                                           205 ---FHITGAYLLYLNHLGLLLL----VLHY--FVELLSHMCGLFYFSDEKYQKGISLWAI 255
                                                                                                                                                                                                                                                                                                                                                                                                            256 V--FILGRLVTLIVS---VLTVGFHLAGSQNRNPDALTGNVNVLAAKIAVLSSSCTIQAY 310
                                                                                                                                                                                                                                                                                                                                                                                                                            297 SRHYLESKILKVVVTNAPEIIGGFHL------DVPNGYIFNKPIXIAFILLFFLQL- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-93255906; Pubmed-8488728;
MEDLINE-93255906; Pibmed-8488728;
Boyer J., Pascolo S., Richard G.F., Dujon B.;
Sequence of a 7.8 kb sequent on the left arm of yeast chromosome XI reveals four open reading frames, including the CAPI gene, an introncontaining gene and a gene encoding a homolog to the mammalian UOG-1
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                  78 AICFACLLSPSLRPYAEPFIFLSYKQPDGS---YGKGPKDACFPIFWVIVFTAFRVIVMD 134
                                                                                                                                                                                                                                                                                                            151 LIWKARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKK---QDIPRQLVYIGLHL--- 204
                                                                                                                                                                                                          47 SIVFLTLQHSVAVPAAE------EQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQE 99
                                                                                                          EDEEASSTNEDK -> GRRGGEFNE (IN REF. 1).
DC00FB5C2D2F22CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                     70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 49.0 kDa protein in UFD4-CAP1 intergenic region.
YKL008C OR YKL156.
                                                                                                                                                          6.7%; Score 128; DB 1; Length 390;
22.0%; Pred. No. 0.0022;
Live 52; Mismatches 119; Indels
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                                                                                                                                                                                   68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
           16
83
137
175
175
221
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221
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Keast 9:279-287(1993).
                                                                                                                     390 AA;
                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----LIYIW 352
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| ransmembrane
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P28496;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 TLQHSVAVPAAEEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 GLLLLV-----LHYFVELLSHM-CGLFYFSDEKYQKGISLWAIVFILGR---LVTLIV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 EATKNDSDLVKKIWFSFREISYRHAWIAPLMILIAVYSAYFTSG----NTTKTNVLHRFV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 TNPFLFKVFYLGQAAFWAQQACILVLQLEKPRKDHNELTFHHIVTLLLIWSSYVFHFTKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 MMTFQMKFFYISQLAYWFHAFPELYFQKTKKQDIPRQLVYIGL-HLFHITGAYLLYLNHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 42.4 kDa protein C3E17.15c in chromosome II. SPBC3E7.15C OR SPBC4F6.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=972;
Lyne M., Wood V., Rajandream M.A., Barrell B.G., Brown D
Churcher C.M.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL. 7691BA623AC0460A CRC64;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.4%; Score 123.5; DB 1; ilarity 19.4%; Pred. No. 0.0056; Conservative 59; Mismatches 117;
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NU4M_FELCA
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                                                                                                                                                                                                                                                                                                                                                                        8,
                                  Skelton J., Churcher C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             57 VAVPAAEEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQF-TKAK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 YPIPGT-----NPAQYGKGRLDIAFCLFYALFFTFCREFIMQEIIARIGRHFNIRAPAK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 LRRFEEQAYTCLYFTVMGSWGLYVMKQTPMWFFNTDAFWEEYPHFYHVGSFKAFYLIEAA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 QNKFNESGQFSVFYFFSCIWGTFIL-ISENCLSDPTLIWKARPHSMMTFQMKFFYISQLA 174
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                              2 GLRKKSTKNPPVLSQEFILQNHAD--IVSCVGMFFLLGLVF---EGTAEASIVFLTLQHS 56
                                                                                                                                                                                                                                                                                                                                                                                                                    GRRRRSKSIVGRAAQNAVLRSKEKTWIVPLILLTLLVGWYFVNPNGYIKYGI-FL----S 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20445173; PubMed=10993077; Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS."; Nature 407:81-86(2000).
                                Gwilliam R., Rajandream M.A., Barrell B.G., Skelton J., Churcher
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-! SUBCELLUIAR LOCATION: Integral membrane protein (Potential).
-! SIMILARITY: BELCOMGS TO THE LASS! FAMILY.
                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                 Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
L6-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADH dehydrogenase I chain L (EC 1.6.5.3) (NADH-ubiquinone
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 YWFHAFPELYFQKTK-KQDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLV
                                                                                                                                                                                                                                                                                                              82FCF8EA6638849A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                               ; Score 116.5; DB 1;
; Pred. No. 0.019;
41; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614 AA
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POTENTIAL.
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                                                                                                                                                                                      EMBL; AL023534; CAA19018.2; -. EMBL; AL031534; CAA20722.2; -.
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155
195
233
270
329
384 AA;
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           FROM N.A.
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Best Local S:
Matches 50
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                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                   SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: TO POLYPEPTIDE 5 OF THE NADH-UBIQUINOL OXIDOREDUCTASE OF CHLOROPLASTS OR MITOCHONDRIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYFQKTKKQDIPRQLVYIGLHLFHITGAYL-----LYLNHLGL----LLLVLHYFVELL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHMCGLFYFSDEKYQKGISLWAIVFILGRL--VTLIVSVLTVGFHLAGSQNRNPDALTGN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 WGTFILISENCLSDPTLIWKARPHSMMTFQMKF------FYISQLAYWFHAFPE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 WYMRYKEGOS--RFFAYTULFIASMSVLVLADNFLFWYLGWEGVSVCSYLLIGFYYTELK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 LATVFF---YMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNESGQFSVF--YFFSCI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSIIFFIILFPLIGFLFLSTIQDFIFKRYTLNI------GIFSIFISFFITCF 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Complete proteome.
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                          CONSTITUTE THE MEMBRANE SECTOR OF THE COMPLEX (BY
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SUBUNIT: COMPOSED OF 13 DIFFERENT SUBUNITS. SUBUNITS NUOA,
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-----KAFILTRVSDVFLMIGMFLI-YREFNSFN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 VNVLAAKIAVLSSSCTIQAYVTWNLITLW------LQRWVEDSNI 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----FQEIKFLSSFLNVENFYYLDYITLFLLLGVIGKSAQLPLQTWLSDAMV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18CCC2DFC4FE27E0 CRC64;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MTND4 ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
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20.2%; Pred. No. 0.043;
ive 52; Mismatches 91;
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InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1_N.
Pfam; PF00361; Oxidored_q1; 1.
Pfam; PF00662; oxidored_q1, 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAD; Ubiquinone;
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Best Local Similarity 20.2's
Matches 59; Conservative
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227
291
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372
410
455
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                          K, L, M, N SIMILARITY)
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STRAIN-K12 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 ----IPRQLVYIGLHLFHITGA----YLLYLNHLGLLLLVLHYFVELLSHMCGLFY--- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| |: || :| || :| || 68 LITWILDILIMIMASQSHLSKETPSRKKIXITMUTLLQILLIMIFTATELI-----MFYILF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 TFILISENCLSDPTLIW-KARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKKQD--- 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 EATLIPTLIIITRWGDQTERLNAGLYFLFYTLVGSLPLLVALLYI-----ON----T 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----FSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDAL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 TGTLNFLIIQYWAKPIS-----TTWSNIFLWLACMMAFMVKMPLYGLHLWLPKAHVEA 223
                                                                                                                                       (Numt) in
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TAMLMPWTCLSRPNMIWINSTIYSLLISLISLSYLNQLGGHSLNFSLLFFSDSLSAPLLV
                       Chordata, Craniata, Vertebrata, Euteleostomi,
Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                            catus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67;
                                                                                                                                                                        !- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol
                                                                                                                                                                                                                                                                                                                                                                                                                                          5.5%; Score 106.5; DB 1; Length 459; 21.3%; Pred. No. 0.15;
                                                                                             MEDILNE-96301400; PubMed-8660972;
Lopez J.V., Cevario S., O'Brien S.J.;
"Complete nucleotide sequences of the domestic cat (Felis
mitochondrial genome and a transposed mtDNA tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                      C1FA567606F1BFB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82;
                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 459 AA; 51497 MW; C1FA567606F1BFB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484 AA
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Interpro: IPR001750; Oxidored_q1.
Interpro: IPR000260; Oxidored_q5_N.
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STRAIN-K12 / MG1655;
MEDLINE-95334362; PubMed-7610040;
                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00361; oxidored_q1; 1.
Pfam; PF01059; oxidored_q5_N; 1.
PRINTS; PR01437; NUOXDRDTASE4.
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16-0CT-2001 (Rel. 40, Last annol
Putative transport protein sgaf.
SGAT OR B4193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
Felis silvestris catus (Cat).
                                                                                                                                                                                                                                                                                                    EMBL; U20753; AAC48578.1; -
                                                                                                                                                  nuclear genome.";
omics 33:229-246(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                         SEQUENCE FROM N.A.
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                                                WCBI_TaxID=9685;
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P39301;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .08 RMQFTKAKQNKFNESGQFSV--FYFFSCIWGTFIL-----ISENCLSDPTLIWKA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 IRTIMLTGHIMFQQAGLIAVTLFIFGYSMWTTIICTAILVSLYWGITSNMMYKPT---- 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reizer J., Charbit A., Reizer A., Saier M.H. Jr.;
"Novel phosphotransferases system genes revealed by bacterial genome
analysis: operons encoding homologues of sugar-specific permease
domains of the phosphotransferase system and pentose catabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Sci. Technol. 1:53-75(1996).
--- FUNCTION: COULD ACT AS THE TRANSPORT PROTEIN FOR THE UNKNOWN
PENTITOL SUBSTRATE OF THE SGA OPERON.
---- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vinket J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAEEDAEKOLAEOSA -> AOKKMOKNNWONSLLNKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 NPPVLSQEFILQNHADIVSCVGMFFL---LGLVFEGTAEASIVFLTLQHSVAVPAAEEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 TGSKSLYYYGVKD-----LAT----VFFYMLVAIIIHATIQEYVLDKINK
                                                    "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IN REF. 1).
2CBEBD0044BC6CAC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SIMILARITY: TO M.PNEUMONIAE SGAT HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Inner membrane;
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W.
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                                                                                                                                                                            REVISIONS TO C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140
                                                                                                                                                                                                       MG1655,
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nes 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Potential).
                                                                                                                                                                                                                                                                                                                                                        Mau B., Shao Y.;
                              Blattner F.R.;
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DOMAIN
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                                                                                                                                                                                                                                                                                                      Sodium- and chloride-dependent glycine transporter 1 (GlyT1) (GlyT-1).
                                      ---QEVTDGCGFSIGHQQQFASWI-AYKVAPFLGKKEESVEDLKLPGWLNIFHDNIVSTA 256
                                                                     271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- ALTERNATURE PRODUCTS: 3 ISORORMS; GLYTT-1A, GLYT-1B AND GLYT-
1C (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-:- TISSUE SPECIFICITY: ALL GLYT-1 SUBTYPES CAN BE FOUND IN BRAIN,
KIDNEY, PANOREAS, LUNG, PLACENTA, LIVER. BUT GLYT-1C SUBTYPE IS
ONLY FOUND IN THE BRAIN.
-:- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: Terminates the action of glycine by its high affinity sodium-dependent reuptake into presynaptic terminals. May play a role in regulation of glycine levels in NMDA receptor-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; 1.
PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; 1.
PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
Neutotransmitter transport; Transport; Transmembrane; Glycoprotein; Symport; Amino-acid transport; Alternative splicing.

DOMAIN 1 94 CYTOPLASMIC (POTENTIAL).
             RPHSMMTFQMKFF--YISQLAYWFHAFPELYFQKTKKQDIPRQLVYIGLHLFH--ITGAY
                                                                    LLYLNHLGLLLLVLHYFVELLSHMCGLFYFSDEKYQKGISLWAIVFILGRLVTLIVSVLT
                                                                                                 257 IVMTIFFGAIL--LSFGIDTVQAMAGKVHWTVYILQTGFSFAVAIFIITQGVRMFVAELS
                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim K.-M., Kingsmore S.F., Han H., Yang-Feng T.L., Godinot N., Seldin M.F., Caron M.G., Giros B., "Cloning of the human glycine transporter type 1: molecular and pharmacological characterization of novel isoform variants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosomal localization of the gene in the human and mouse
                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                  692 AA.
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Pfam; PF00209; SNF; 1.
PRINTS; PR00176; NANEUSMPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                              272 VGFHLAGSQNRNPDALTGNVNVLAAKIAVLSS 303
                                                                                                                                                           315 EAFN-GISORLIPGA-----VLAIDCAAIYS 339
                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;
MEDLINE-94239375; PubMed-8183239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pharmacol. 45:608-617(1994).
                                                                                                                                                                                                                                                             (Rel. 33, Created)
(Rel. 33, Last sequ
(Rel. 40, Last anno
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                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurotransmission
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAMILY (SNF).
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606
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01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 601019;
                                                                                                                                                                                                                                                                                          16-OCT-2001
                                                                                                                                                                                                                   S6A9_HUMAN
ID S6A9_HUMAN
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Mol. Phar
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14;
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MAAAHGPVAPSSPEQVTLLPVQRSFFLPPFSGATPSTSLAE
                                                                                                                                                                                                                                                                                                                        SVLKVWHGAYNSGLLPQLMAQHSLAMAQ -> MVGKGAKGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97197983; PubMed-9046099; Voet M., Defoor E., Verhasselt P., Riles L., Robben J., Volckaert G.; Voet M., Defoor E., Verhasselt P., Riles L., Robben J., Volckaert G.; The sequence of a nearly unclonable 22.8 kb segment on the left arm chromosome VII from Saccharomyces cerevisiae reveals ARO2, RPL9A, TIP1, MRF1 genes and six new open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 YMLVAIIIHATIQEYVLDKINKRM--QFTKAKQNKFNESGQFSVFYFFSCIWGTFILIS- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKKQDIPRQL 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 LLGCLGVSWL-----TATFPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 IVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVPAAEEQATGSKSLYYYGVKDLATVFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 VVLTILFVRGVTLEGAFDGIMYYLTPQWDKILEAKVWGDAASQIFYSLACAWGGLITMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ILGRLVTLIV------SVLTVGFHLAGSQNRNPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 VYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFYFSDEKYQKGIS----
                                                                                                                                                                                                                                                                 (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycoties;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID-4932;
                                                                                                                                              10 (POTENTIAL).
11 (POTENTIAL).
12 (POTENTIAL).
12 (COTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91; Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-ULL-1999 (Rel. 38, Last annotation update)
Hypothetical 90.8 kDa protein in HUL5-SEC27 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 692;
                                                                                                                                                                                                                                                                                                                                                         MISSING (IN ISOFORM GLYT-1B). FABA3243A0D98073 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 YNKFHNNCYRDSVII--------SITNCA-----
                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                              ISOFORM GLYT-1A)
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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Similarity 19.3%; Pred. No. 0.57;
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                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                        (POTENTIAL).
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                                   (POTENTIAL)
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76823
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1186
2733
3192
3318
3318
3318
371
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693
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                                                                                                                                                                                                                                                                                                                                                             16
692 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 LWAIVF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
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P53121;
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Best Local Si
Matches 64;
                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
SEQUENCE
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CARBOHYD
VARSPLIC
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CYB_PARTE
P15585:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGQFSVFYFFSCIWGTFILISENCLSDPTLI -----WKARPHSMMTFQ---MKFFYI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: | : : : : : | : CTGFTFFVLCGYVLAGFIIVFKCCVELATRLGWIQKARFWEFRKQWRMILKGALLRYIYI 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LGLVFE-----46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---QATGSKS 71
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                                                                                                                                                                                                                                                                                                             Yeast 12:887-892(1996).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO YEAST YALO53W AND S.POMBE SPACIF7.03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 134; Indels 144;
                                                                                                                                                        Escribano V., Eraso P., Portillo F., Mazon M.J.;
"Sequence analysis of a 14.6 Kb DNA fragment of Saccharomyces cerevisiae chromosome VII reveals SEC27, SSMLb, a putative S-adenosylmethionine-dependent enzyme and six new open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FHLAGSQNR------303
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19.3%; Pred. No.
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                                                                                          STRAIN-S288C / FY1679;
MEDLINE-96437978; Pubmed-8840506;
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                                                             SEQUENCE OF 616-802 FROM N.A.
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EMBL; Z72660; CAA96850.1; -.
EMBL; X92670; CAA63357.1; -.
SGD; S0003107; YGL139W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X99960; CAA68223.1; -.
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Yeast 13:177-182(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.

SUBBURIT: THE MAIN SUBBURITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN.

SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000179; Cyt_b_b6.
Pfam: PF00013; cytcohrome_b_N: 1.
PR03ITE; PS00192; CYTOCHROME_B_HEME; FALSE_NEG.
PROSITE; PS00193; CYTOCHROME_B_O): FALSE_NEG.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 18:173-180(1990).
-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX II OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 WGTFILISENCLSDPTLIWKARP-HSMMTFQMKFFYISQLAYWFHAFPELYFQKTKKQDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pritchard A.E., Seilhamer J.J., Mahalingam R., Sable C.L., Venuti S.E., Cummings D.J.; "Nucleotide sequence of the mitochondrial genome of Paramecium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FFGLVLCCTH-LSEITLITIAANIFHTFFMFKGK-----AYWF-----LFTDKQLNTDT
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                                                                                                                                                                                                                                                     Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66
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IRON 2 (HEME B566 AXIAL LIGAND).
IRON 2 (HEME B562 AXIAL LIGAND).
IRON 1 (HEME B566 AXIAL LIGAND).
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21.5%; Pred. No. 0.59;
ive 58; Mismatches 131; Indels
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                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
391
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90174913; PubMed=2308823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46044 MW;
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                                                                                                                                                                                                Paramecium tetraurelia. Mitochondrion.
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86
173
187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
86
173
187
                                                                                                                                         Cytochrome B.
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                                                       01-APR-1990
                                                                                                                                                                   COB OR CYTB
                                                                                                                                                                                                                                                                                  Paramecium
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                                  207 EMLWWDEALSNELTNFFVLLV-FITLAFFLLFEE---PEALSYEIFWWGDIGLSTDVRFY 262
                                                                                                 263 GVAPHWYFRPFWAMLIACPFHKTGIFGLLFFFVTLYYQPNLHGVSDQNSYGKKTLFISST 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95350630; PubMed=7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Karlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Witterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Futhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE CYSTW
             --LW---AIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALT-----GNVNVLA-AKIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infect. Immun. 62:4515-4525(1994).
-!- FUNCTION: INVOLVED IN A PERIPLASMIC BINDING-PROTEIN-DEPENDENT
IRON(III) TRANSPORT SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95012644; pubMed-7927717; sanders J.D., Cope L.D., Hansen E.J.; "Identification of a locus involved in the utilization of iron by Haemophilus influenzae.";
                                                                              VLSSSCTIQAYVTWNL------ITLWLQRWVEDSNIQASCMKKKRSRSS-
                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                 P71338; 053440;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1ron(III)-transport system permease protein hitb.
HITB OR HI0098.
                                                                                                                                                                                                                                                                   506 AA.
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EMBL; S72674; AAB32111.1; -.
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Pfam; PF00528; BPD_transp: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995)
                                                                                                                                                                                                                                                                     STANDARD;
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362 ALSLVYFSIH-----YANDLYQTFFVIIIAYFMLYLPMAQTTLRASLEQLSDQIE 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 AALLSAVLMAICILIVF----GEIFFRGKQTLYHSGKGVTRPYLVKTLSFGKQCLTFGF 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 KDLATVFFYML---VAIIIHATIQEYVLDKINKRMQFTKAKQNKFNESGQFSVFYFFSCI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WGTFILISENCLSDPTLIWKA-RPHSMMTFQMKFFYISQLAYWFHAFPELYFQKTKKQDI 193
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   24 ADIVSCVGMFFLLGLVFEGTAEASIVF---LTLQHS---VAVPAAEEQATGSKSLYYYGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 PRQLVYIGLHLFHITGAYLLYLNHL -- GLLLLLVLHYFVELL ----- SHMCGLFYFSDEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVGQSLGRNPFYIFRTLTL--------PAILPGVAAAFALVFLNLMKELT
                                                                                                                                                                                                                                                                                                                                                                                                   81;
                                                                                                                                                                                                                                                                                                                                                                     Length 506;
Iron transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                   5.1%; Score 98.5; DB 1; Length 5
23.7%; Pred. No. 0.78;
tive 36; Mismatches 131; Indels
                                                                                                                            POTENTIAL.
POTENTIAL.
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F -> L (IN STRAIN TN106).
G -> C (IN STRAIN TN106).
V -> G (IN STRAIN TN106).
T -> M (IN STRAIN TN106).
T -> M (IN STRAIN TN106).
W; ADA28861C1481AID CRC64;
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Matches
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15;

6, 2002, 17:21:15 Search completed: September 633 sec Job time:

Pfam; PF00528; BPD\_transp; 2. PROSITE; PS00402; BPD\_TRANSP\_INN\_MEMBR; FALSE\_NEG.

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September 6, 2002, 17:20:26 ; Search time 80.19 Seconds
(without alignments)
796.048 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                       OM protein - protein search, using sw model
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US-09-807-470-4 1920 1 MGLRKKSTKNPPVLSQEFIL.....VGVETSNRVDCPPKRKEKSS 369 Title: Perfect score: Sequence:

562222 seqs, 172994929 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

%p\_human:\*
sp\_invertebrate:\*
sp\_invertebrate:\*
sp\_mhc:\*
sp\_phage:\*
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sp\_purus:\*
sp\_virus:\*
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sp\_virus:\*
sp\_vortebrate:\*
sp\_vortebrate sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\* SPTREMBL\_19:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Q91v04 mus musculu	Q90zm0 xenopus lae	Q90zml brachydanio	Q90z19 xenopūs lae	Q924z5 mus musculu	Q9w5c2 drosophila	Q9w5c3 drosophila	Q9u113 drosophila	Q9u3p5 caenorhabdi	Q9xxk7 caenorhabdi	Q9cvj6 mus musculu	Q9d6j1 mus musculu	Q9m6a4 lycopersico	Q9ha82 homo sapien	Q95rn6 drosophila	Q9ldf2 arabidopsis
SUMMARIES			a	Q91V04	Q902M0	Q902M1	Q90ZL9	092425	Q9W5C2	Q9W5C3	Q9U1L3	Q9U3P5	Q9XXK7	09CVJ6	Q9D6J1	Q9M6A4	Q9HA82	Q95RN6	Q9LDF2
				11	13	13	13	11	Ŋ	Ŋ	2	2	Ŋ	11	11	10	4	Ŋ	10
			Match Length DB	374	373	369	371	370	368	1575	368	371	373	159	393	308	394	400	310
	ф	Query	Match	7.07	65.2	58.8	42.7	42.2	31.4	31.4	31.1	25.7	25.4	24.6	8.2	7.6	7.4	7.0	9.9
			Score	1357.5	1251	1129	820	811	602.5	602.5	597.5	464	487	472.5	156.5	146.5	143	134.5	127
		Result	No.	н	~	m	4	S	9	7	80	σ	10	11	12	13	14	15	16

091jk3 arabidopsis 09m6a2 arabidopsis 096g23 home sapien 098k18 rhizobium 1 0924z4 mus musculu 09xwe9 caenorhabdi 09yv7 palocynthia 09yv7 palocynthia 09tw14 caenorhabdi 09tw14 caenorhabdi 09tw14 caenorhabdi 09tw14 caenorhabdi 09tw14 caenorhabdi 09tw14 caenorhabdi 09tw14 caenorhabdi 09tw15 mus musculu 09d6k9 mus musculu 09d6k9 mus musculu 09d8p5 naegleria g 09u17 f home sapien 09116 rickettsia 091269 arabidopsis 091269 arabidopsis 09127 carnobacter 0998p4 naegleria g	099h57 drosophila 09fel8 medicago tr 032204 bacillus su 09861 malawimonas 091yr7 arabidopsis 035716 romanomermi 09sya2 arabidopsis
296 10 Q9LJK3 297 10 Q9M6A2 380 1 Q9M6A2 380 11 Q924A4 360 5 Q9XWE9 3724 5 Q9CVB8 378 5 Q9YIV7 371 5 Q9XU34 402 8 Q9T6M3 60 17 Q9JKM1 414 11 Q9D6K9 414 11 Q9BCK9 414 11 Q92A23 339 5 Q9WA23 642 4 Q9UN76 642 4 Q9UN76 642 4 Q9UN76 642 4 Q9UN76 643 10 Q9FZ69 308 10 Q9FZ69 310 8 Q9GBP5 50GRP5 642 4 Q9UN76 643 10 Q9FZ69 310 8 Q9GBP6 50GRP6 50GRP6 50GRP6 50GRP7 50GRP6 50GRP6 50GRP6 50GRP6 50GRP6 50GRP6 50GRP6 50GRP7 50GRP6 50GR	10 10 10 10 10
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116.5 116.5 111 111.5 111.1 106.5 100.5 100.5 100.5 100.5 98.5 98.5	97. 96. 96. 96. 96. 8. 8.
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#### ALIGNMENTS

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FNESGOFSVFYFFSCIWGTFILLSENCLSDPTLIWKARPHSMMTFOMKFFYISOLAYWFH 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGLRKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVP 60
                                                                        01-DEC-2001 (TEMBLEL. 19, Last sequence update)
01-DEC-2001 (TEMBLEL. 19, Last annotation update)
17RAM.
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cypriniformes; Cyprinidae; Danio.
NCBL_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 FYFSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 AFPELYFQKTKKQDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGL
                                                                                                                                                                                                                                                                                                                              58.8%; Score 1129; DB 13; Length 369; 58.2%; Pred. No. 2.1e-95; ive 64; Mismatches 84; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hartmann E.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY029535; AAK40303.1; -.
SEQUENCE 371 AA; 43548 MW; 582231A5286D130B CRC64;
                                                                                                                                                                                                                                                 Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY029529; AAK40297.1; --
SEQUENCE 369 AA; 41743 MW; A3EE6263E3165846 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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                               369 AA
                                                              Created)
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                            (TrEMBLrel. 19, (TrEMBLrel. 19,
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Best Local Similarity
Matches 217; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                              01-DEC-2001
                                                                                                                                                                                                                                       Hartmann E.;
                                            Q90ZM1;
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                               Q90ZM1
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                                                                                                          61 AAEEQATGS-KSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 NESGQFSVFYFFSCIWGTFILISENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 FPELYFQKTKKQDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLF 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 YFSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAKIA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESGQLSAFYLFACVWGTFILISENYISDPTILWRAYPHNLMTFQTKFFYISQLAYWLHAF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 VLSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKK----RSRSSKKRTENGV-GVET 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGLRKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKK----RSRSSKKRTENGV-GVETS
                                                                                             FSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAKIAV
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6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY029534; AAK40302.1; --
SEQUENCE 373 AA; 43121 MW; 62AFA9E9859769DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -.
; 62AFA9E9859769DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.2%; Score 1251; DB 13;
63.7%; Pred. No. 1.4e-106;
ive 53; Mismatches 75;
                                                                                                                                                                                                                                                                                                                               373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                     356 NRVDCPPKRKEKSS 369
                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
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Best Local Simil
Matches 239; C
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RESULT Q902M0

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176 PELYFOKVRKEEVPROLOYICLYLLHITGAYLLNLSRLGLILLLLQYSTEALFHMARLFH 235
                         241 FSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAKIAV
                                                                                                                                                                                                          368 AA.
                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                          PRT;
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FlyBase; FBgn0040340; EG:BACR7A4.5.
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                                                                                                                                              355 KAENGTSSRTKK 366
                                                                                                                      353 ETSNRVDCPPKR 364
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                    SSIQTLD----GEILYYHYGVKDLVTILFYVVIAIILHAIVQEYILDKINKRLHLSKVKQ 110
                                                                                                                                                                                   SPENESGQLAAFHLASMFWCLYVSATEGYLSYPKTLWESYPHVYLPFQVKFFYLCQLAYW 170
                                                                                                                      57 VAVPAAEEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQETVLDKINKRMQFTKAKQ 116
                                                                                                                                                                     NKFNESGQFSVFYFFSCIWGTFILISENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYW 176
                                                                                                                                                                                                                    177 FHAFPELYFQKTKKQDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMC 236
                                                                                                                                                                                                                                  295 AAKIAVLSSSCTIQAYVTWNLITLWLQRWVEDSNIQAS------CMKKKRSRSSKKRT- 346
                                                                                                                                                                                                                                                                                                                                          289 LFRMVVLLLIMCVSQTWMMRRIHFQLRRWRECCKEQAARKRSVAVAMMKQQAKVIKRESG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AAEEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESGQFSVFYFFSCIWGTFILISENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 PELYFOKTKKODIPROLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLFY 240
                                                                                                                                                                                                                                                                    GLFYFSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQ -- NRNPDALTGNVNVL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                      1 MGLRKKSTKNPPVLSQEFILQNHADIVSCVGMFF----LLGLVFEGTAEASIVFLTLQHS 56
                                                                                    1 MGLRKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVAVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAFRRR-TKSYPLFSQEFIIHNHADIGFCLVLCVLIGLMFEVTAKTAFLFILPQYNISVP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                30;
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                      Score 820; DB 13; Length 3 Pred. No. 4.5e-67; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY029530; AAK40298.1; -- SEQUENCE 370 AA; 43182 MW; F8E768AFB0582548 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 AA.
                                                                                                                                                                                                                                                                                                                                                                   -- ENGVGVETSNRVDCPPKRKEKS 368
                                                                                                                                                                                                                                                                                                                                                                                         349 YHENGV-VKAENG-STPROKKIKS 370
                                              73;
                                  44.38;
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Matches 159; Conservative
                                              Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                      Query Match
Best Local S
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Bashurner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Bardon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Ffeiffer B.D.,
RA Maril J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RA Beeson K.Y., Bearos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benco P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis R.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dallike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallike C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dulkov B.C., Dun, P.
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Glabar P., Harris M.,
RA Hustin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Wei M.-H., Ibegwam C.,
RA Minnel B.E., Kodirac C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Rateri B., McIntosh T.C., McLeod M.P., Nickon K.,
Rhamel B.E., Kodirac C.D., Kraft C., Kratt C., Kratt M., Manny D.M., Nelson D.L.,
Rhamel B.E., Wolyne N., Nixon K., Nusskern D.R., Pacleb J.M.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Santh T.,
Shue B.C., Siden Klamoz I., Sanpson M., Stupski M.P., Santh T.,
Shue B.C., Siden Klamoz I., Sanpson M., Stupski M.P., Santh H.,
Shue B.C., Siden Klamoz I., Sanpson M., Stupski M., San B.,
Spier E., Spradling A.C., Zaveri J.S., Zhan M., Zhu S.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                      354
                                                                                                                                                                                                   LSSSCTIQAYVTWNLITLWLQRWVE-----DSNIQASCMKKKRSRSSKKRT---ENGVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
EG:BACR7A4.5 PROTEIN.
EG:BACR7A4.5 OR CG11642.
EG:BACR7A4.5 OR CG11642.
EG:BACR7A4.5 W CG11642.
ELSEMPRIA melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
George R.A., Lewis S.E., Holf R.A, Poskins R.A., Galle R.E.,
George R.A., Lewis S.E., Holf W., Hoskins R.A., Galle R.E.,
A George R.A., Lewis S.E., Taichards S. Ashburner M., Henderson S.N.,
By Sutton G.G., Wortman J.R., Yandeall M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Brandon R.C., Rayter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bulck J., Brotstein P., Brottler P.,
A Burtis K.C., Busam D.A., Bullek C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Harris N.L., Harvey D., Heilman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
                                                                                 8
                                                                                                                                                                                                   GQFSVFYFFSCIWGTFILISENCLSDPTLIWKARPHSMMTFQMKFFYISQLAYWFHAFPE 182
                                                                                                                                                                                EEQATGSKSLYYYGVKDLATVFFYMLVAIIIHATIQEYVLDKINKRMQFTKAKQNKFNES 122
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CG18890 NR CG16994.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota, Neoptera; Endopterygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                              298 IAVLSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKKRSRSSKKRTENGVGVETSNR 357
                                                                                                                4 RKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQHSVA-VPAA 62
                                                                                                                                 LYFQ -- KTKKQDIPRQLVYI-GLHLFHITGAYLLYLNHLGLLLLVLHYFVELLSHMCGLF
                                                                                                                                                                                                                                                                                                                                                                               --YFSDEKYQKGISLWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALTGNVNVLAAK
                                                                                                                                                                                                                                                                                                                                                                                                             247 GVFDREERLAKLRVVNNAVFFLIRFATSVIGVLTLYYGIGGVRS-------
                                                                                 41;
                                                 Length 368;
                                                                                   Indels
 693794394C2ED787 CRC64;
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Last annotation update)
                                                                               63; Mismatches 132;
                                                 Score 602.5; DB 5
Pred. No. 3.9e-47;
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41780 MW;
                                               31.4%;
36.9%;
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                                                                                 Conservative
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01-DEC-2001 (TrEMBLrel.
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 368 AA;
                                               Query Match
Best Local Similarity
Matches 138; Conserv
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01-MAR-2001
 SEQUENCE
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Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lakor D., Lei Y., Lei Y., Levitzky A.A., Lij J., Liž Z., Liang Y., Lin X., Lai X., Lei Y., Lei Y., Lei Y., Lei Y., Laing Y., Lin X., Lai X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mornt S.M., Moy M., Murphy B., Murphy D.M., Nelson D.E., Ra Melson D.R., Nalson K.A., Nixon S., Pollard J., Puri V., Reese M.G., Rainest K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Reinert K., Stennelton S., Panders R.D.C., Scheeler F., Shen H., Rainest K., Stennelton M., Strong R., Sun E., Spier E., Siden-Kiamos I., Simpson M., Stkopski M.P., Smith T., Ray Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., R. Johny K.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., A Zheng X.H., Myers E.W., Rubin G.M., Venter J.C., The genome sequence of Drosophila melanogaster.", Smith H.O., R. Schole 299512085-209512000.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EG:BACR7A4.5 PROTEIN.
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1575 AA; 172376 MW; 2F8C0E528B67CD69 CRC64;
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C24F3.1B PROTEIN.
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357 EKKRQDS
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                           Louis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Papagiannakis G., Spanos L., Bolshakov V., Siden-Kiamos I., Louis "Sequencing the distal X chromosome of Drosophila melanogaster."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                        Length 368;
                                                                                                                                                                                                                                                                                   31.1%; Score 597.5; DB 5; Length 36.6%; Pred. No. 1.1e-46; ive 63; Mismatches 133; Indels
                                                                                                                              Benos P.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL109630; CAB65875.1; -.
FlyBase; FBGn0040340; EG:BACR7A4.5.
SEQUENCE 368 AA; 41766 MW; 693795FFFC2ED4A6 CRC64;
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Science 282:2012-2018(1998).
EMBL: AL022716: CAL187C...;
InterPro: IPR001185; MSCL.
SEQUENCE 371 AA; 42420 MW; 5269FC7231222592 CRC64;
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Best Local Similarity 36.6%
Matches 137; Conservative
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337 AKTPKDKVKRKKES 350
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Caenorhabditis elegans.
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SEQUENCE FROM N.A.
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7 GSKASKKPQPPILSHEFIIQNHGDIMSCVVMVFIVGLMFPLTHSLSSLFIAPQYNGTYTV 66
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                           2 GLRKKSTKNPPVLSQEFILQNHADIVSCVGMFFLLGLVFEGTAEASIVFLTLQ----HSV
                                                                                                                                                                                                                                                                                                 KFNESGQFSVFYFFSCIWGTFILISENC -- LSDPTLIWKARP -- HSMMTFQMKFFYISQL
                                                                                                                                                                                                                                                                                                                                                                                                 174 AYWFHAFPELYFQKTKKQDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HMCGLFYFSDEKYQKGIS----LWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPDALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 HIARFAHFVG---RKGLSDPAFKLFNGSFVLVRLGSIIIAVMTFWYGLRQAESPFVDISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNVNVLAAKIAVLSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKKRS-----RS
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  Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42655 MW; 92D65DF05F50B9CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
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25.7%; Score 494; DB 5; 32.4%; Pred. No. 3.5e-37; ive 74; Mismatches 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 AA
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MEDLINE=99069613; PubMed=9851916;
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Science 287:2012-2018(1998).
EMBL; ALO22116; CAA18772.1; -.
InterPro; IPR001185; MSCL.
SEQUENCE 373 AA; 42655 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
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                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                         Similarity
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336 KK----RSRSSKKRTENGV-GVETSNRVDCPPKRKEKSS 369

qq

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1 NHLGLVLLVLHYFVEFLFHISRLFYFSDEKYQKGFSLWAVLFVLGRLLTLILSVLTVGFG

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STRAIN-C57BL/63; TISSUE-PANCREAS;

KRANING-27BL/64; TISSUE-PANCREAS;

KRANING-27BL/64; TISSUE-PANCREAS;

KRANI J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Raito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rochiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Rakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Romstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Rochonstein M.J., Bult C., Ramiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakanoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nyashiav-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nyashiav-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
118 KFNESGQFSVFYFFSCIWGTFILISENCLSD----PTLIWKARP--HSMMTFQMKFFYI 170
                                                                                                                                                                          171 SQLAYWFHAFPELYFQKTKKQDIPRQLVYIGLHLFHITGAYLLYLNHLGLLLLVLHYFVE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 LLSHMCGLFYFSDEKYQKGIS----LWAIVFILGRLVTLIVSVLTVGFHLAGSQNRNPD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 ALTGNVNVLAAKIAVLSSSCTIQAYVTWNLITLWLQRWVEDSNIQASCMKKKRS----- 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse),
Sukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 1810049E02RIK PROTEIN (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last and
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MGD; MGI:1919515; 1810049E02Rik.
NON_TER
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STRAIN-C57BL/65; TISSUB-HIPPOCAMPUS;

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konoo H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Raito T., Okazaki Y., Gojobori T., Banoo H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Shunorer M., Eatalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Futuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Ruconstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Ry Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakanoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Whynshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordonis A., Wang K., Hasegawa Y., Kawaji H., Kohtsuki S.,

"Functional annotation of a full-length mouse cDNA collection.";

Nature 409:685-690(2001).

Hayashizaki Y.;

to the EMBL/GenBank/DDBJ databases

Submitted (FEB-2001)

Strausberg R.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Mus musculus (Mouse). Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI\_TaxID=10090;

SEQUENCE FROM N.A.

01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 2900019C14RIK PROTEIN (RIKEN CDNA 2900019C14 GENE) (TRH1).

2900019C14RIK.

Created) PRT;

01-JUN-2001 (TrEMBLrel. 17,

PRELIMINARY;

090631 RESULT 12

09D6J

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107 KRMQFTKAKQNKFNESGQFSVFYFFSCIWGTFILISENCLSDPTLIWKARPHSMMTFQMK 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.2%; Score 156.5; DB 1
26.7%; Pred. No. 3.2e-06;
iive 38; Mismatches 73
SM00389; HOX; 1,
E; PS50071; HOMEOBOX_2; 1
CE 393 AA; 46016 MW;
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Best Local Similarity
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Gaps

5;

DB 11; Length 159; Indels

24.6%; Score 472.5; DB 11; ilarity 61.6%; Pred. No. 1.2e-35; Conservative 19; Mismatches 37;

Similarity

Query Match Best Local Simil Matches 98; C

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Hartmann E.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (ARP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK013554; BAB28903.1; -.
EMBL; AX029531; AAR(0299.1; -.
MKD; MX1:1914510; 2900019C14Rik.
InterPro; IPR001356; Homeobox.

B2038F7A128F816F CRC64;

SMART; SM PROSITE; 3 SEQUENCE

5,

Gaps

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223

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**09M6A4** RESULT 13

1D ACC DDT ACC

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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID-7227;
                                                                                                                                                                            Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 FVELLSHMCGLFYFSDEKYQKGIS----LWAIVFILGRLVTLIVSVLTVGFHLAGSQNRN 283
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 46.4 KDA PROTEIN.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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STRAIN-Y, CN BW SP;
STRAIN-Y, CN BW SP;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
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EMBL; AK022151; BAB13972.1; -.
EMBL; BC0098281; AAH09828.1; -.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 AA; 46398 MW; 67228829BDED2801 CRC64;
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Last annotation update)
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PROSITE; PS5071; HOMEOBOX_2; 1.
HYPOThetical protein. 46398 MW; 6
SEQUENCE 394 AA; 46398 WW; 6
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01-DEC-2001 (TrEMBLrel. 19, La
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TISSUE=LUNG CARCINOMA;
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                    TISSUE-EMBRYO;
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                                           181 WWYLLELGFYLSLLITLPFD-VKRKDFKEQVVHHFVAVGL----IGFSYSVNLLRIGAVV 235
                     FFYISQLAYWFHAFPELYFQKTKKQDIPRQLVY----IGLHLFHITGAYLLYLNHLGLLL 222
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MEDLINE-20243803; PubMed-10781105;
Brandwagt Br., Mesbah L.A., Takken F.L.W., Laurent P.L.,
Rneppers T.J.A., Hille J., Nijkamp H.J.J.;
"A longevity assurance gene homolog of tomato mediates resistance to
Alternaria alternate f. sp. lycoperasici toxins and fumonisin Bi.";
Proc. Natl. Acad. Sci. U.S.A. 97:4961-4966(2000).
EMBL; AF198177; AAR67518.1; -.
SEQUENCE 308 AA; 36301 MW; 2BD3378CE53F416D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic and physical analysis of a YAC contig spanning the fungal disease resistance locus Asc of tomato (Lycopersicon esculentum)."; Mol. Gen. Genet. 261:50-57(1999).
                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum (Tomato). Bubryophyta; Tracheophyta; Streptophyta; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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STRAIN-CV. VFNT CHERRY;
MEDLINE-99168767; PubMed=10071209;
Mesbah L.A., Kneppers T.J., Takken F.L., Laurent P., Hille J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.6%; Score 146.5; DB 10; Length 308; 23.1%; Pred. No. 2e-05;
                                                                                                                               LVLHYFVELLSHMCGLFYFSDEKYQKGIS----LWAIVFILGRLVTLIVSVL 270
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Matches 50; Conservative
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                                                                                                                                                                    Gaps
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Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-201) to the EMBL/GenBank/DDBJ databases.
EMBL; AY601255; AAL28803.1; - ABS86DB2B8111E62 CRC64;
                                                                                                                                                                    85;
                                                                                                                           Query Match 7.0%; Score 134.5; DB 5; Length 400; Best Local Similarity 19.0%; Pred. No. 0.00034; Matches 70; Conservative 68; Mismatches 145; Indels 85
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